

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: June 19, 2004, C1:08:10 ; Search time 5838 Seconds
(without alignments)
3585.934 Million cell updates/sec

Title: JS-09-980-468-2
Perfect score: 2595

Sequence: 1 M A L V T D F L N F L G T T W K S V A V V R K A L K E I A C E A S I R U H A H 483

Scoring table:

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Ygapcp 10.0 , Ygapext 0.5
Fgapcp 6.0 , Fgapext 7.0
Delcp 6.0 , Delext 7.0

Searched:

3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2	2595	100.0	2040	6	AX058830		AX058830 Sequence
3	2595	100.0	2040	8	CPU250734		AJ250734 Ceratodon
4	1619	62.4	2160	6	AX058840		AX058840 Sequence
5	1619	62.4	2160	8	CPU250735		AJ250735 Ceratodon
6	1475	56.8	1578	6	AX481617		AX481617 Sequence
7	1475	56.8	1578	6	AX481946		AX481946 Sequence
8	1475	56.8	2012	6	AX069275		AX069275 Sequence
9	1475	56.8	2012	8	PPAJ2980		PPAJ2980 Physcomit-
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12	1475	56.8	17752	6	AX481638		AX481638 Sequence
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16	852.5	32.9	1521	8	AB070555		AB070555 Mortierel
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24	841.5	32.4	1617	6	BDD092914		BDD092914 Methods a
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37	790	30.4	1380	6	AX467717		AX467717 Sequence
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40	728.5	28.1	1947	8	AF465283		AF465283 Mortierel
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ALIGNMENTS

RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Db 1450 CACGCTCAC 1458

RESULT 2

AX058830 AX058830 2040 bp DNA linear PAT 17-JAN-2001

LOCUS Sequence 1 From Patent WO0075341.

DEFINITION ACCESSION AX058830 GI:12311150

VERSION VERS

KEYWORDS Ceratodon purpureus

SOURCE Ceratodon purpureus

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Dicrachaeae; Ceratodon.

REFERENCE Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and Zaehringen, U.

AUTHORS g (d) 6-acetyljenase and 9 (d) 6-desaturase from ceratodon purpureus

TITLE Patent: WO 0075341-A 1 14-DEC-2000;

JOURNAL BASF AKTIENGESELLSCHAFT (DE)

FEATURES Location/Qualifiers 1. .2C40

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CDS

/note="unnamed protein product"

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ORIGIN

US-09-980-468-2 (1-483) × AX058830 (1-2040)

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		Percent Similarity: 100.00%
		Best Local Similarity: 100.00%
		Query Match: 100.00%
		DB: 6 Gaps: 0

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Qy 21 TyrThrHisSerTyrAlaGlyAsrTyrGlyProThrLeuLysValSer 40

Db 236 TACACCCATAAGCTATGCTGGAAACTATGGCCCTACTTGAAGAACAGTTCT 295

Qy 41 AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSerValGlnAspLysPro 60

Db 296 GCTCAAGGAAACTGGGGACAGACACTGAGACAGAGATCGGTGCGAGCAAAGCCA 355

Qy 61 GlyThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCystrpMetIle 80

Db 356 GGCACTTACTCTGGCCGATGTTGCTTCAGACAGGCCTGAGACTGCTGGATGATC 415

Qy 81 ValLysGluLysValTyrAspIleSerArgPheAlaAspAspPhiAspProGlyThrVal 100

Db 416 GTCAAAGAGAAAGGTGATGATATTAGCGTTTTCGGGAGACCACCTGGAGGACGGTA 475

Qy 101 IleSerThrTyrPheGlyArgAspGlyTyrAspValPheAlaSerIleArgLeu 120

Db 1556 GCCTCTGTCGCGGTTGARGGCSCTCAAGGAATTGCTGATGAACGCTAAATCGACCT 1615

QY	381	SerHisAsnGlyLysGluvaltyrAsnGluSerLysAspPheValArgAlaGlnValIle	400	
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QY	401	ThrThrArgAsnThrLysArgGlyTrpPheAspTrpPheThrGlyGlyLeuAspThr	420	
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QY	421	GlnIleGluHisHisLeuPheProThrMetProArgHisAsnTyrrProLysValSerVal	440	
Db	1436	CAGATGAGSCATCACCTGTTCCAACAATGCCAGGCACAACACTACCCCHGATGCCACCT	1495	
QY	441	GlnvalGluAlaLeuCysLysLysAlaLeuGluTrpTyrrAspSerValAlaSerIleArgLeu	460	
Db	1496	CAGETCGAGGCTCTTGCAAGAAGCAGGGCTCAAGGAAATTGCTGATGARGGTCAATTGGCTT	1555	
QY	461	AlaSerValAlaValLysAlaLeuCysLysLysAlaLeuGluAlaSerIleArgLeu	480	
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DEFINITION	AX358840			
ACCESSION	AX358840.1	GI:12311157		
VERSION				
KEYWORDS				
SOURCE				
ORGANISM	Ceratodon purpureus			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;			
	Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Ceratodon.			
REFERENCE	1			
AUTHORS	Heinz,E., Stymne,S., Lee,M., Girke,T., Sperling,P. and Zaehringer,U.			
TITLE	g(d) 6-acetyl enase and g(d) 6-desaturase from ceratodon purpureus			
JOURNAL	Patent: WO 0075341-A 11-14-DEC-2000;			
BASF AKTIENGESELLSCHAFT (DE)	BASF AKTIENGESELLSCHAFT (DE)			
LOCATION/QUALIFIERS				
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QY	307	PhemetaLaArgTyrrSerTrpThrPheGlySerLeuLeuPheThrPheAsnProAspLeu	326	
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QY	327	SerThrThrLysGlyLeuIleGluLysGlyThrValAlaPheHistYrAlaTrpPheSer	346	
Db	1248	ACCCCTGGCGAGAAGCTTGGAGGGAAACGATGGCTTGCACATTTGGTTAAAT	1307	

Qy	247	ThrLysHisAsnIleHisthrAlaProAsnGluCysAspGluGlnTyrthrProLeu	266	
Db	1008	ACCAAGCACAAACCTGCATCATGGTGTCTCGATGAATGCCAACAAAGTCACACCGATT	1067	
Qy	267	AspGluAspPheAspThrLeuProLeuAlaIleAlaSerLysGluIleLeuAlaThrVal	286	
Db	1068	GATGAGGATATTGATACTCTCCCATCATGGAGTAAGATCTCTGGCCACTGTGTT	1127	
Qy	287	GluSerLysArgIleLeuArgValLeuGlnIleGlnHisthrMetIleLeuProLeuLeu	306	
Db	11128	GAGAGCAAGACCAGATGGTAGTGTGAGTTCTCAGTACAGCACCTATTCTTGGTTCTTTG	1187	
Qy	307	PheMetAlaArgTyrSerIleTrpAlaIleLeuPheAsnProAspLeu	326	
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Qy	347	TrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThr	366	
Db	1308	AGTGTGCGTTTATCTGCTCCCGGA---TGGAAAACCAAGTGGCTATTGGATGGTGTGTCAC	1364	
Qy	367	GluLeuValAlaGlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGlu	386	
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Db	1425	GTTGACAATACGTCAAAGGACTTCGGTGAATGCCAGATGGCATCAGTCACATCAA	1484	
Qy	407	ArgGlyTrpPheAsnAspTrrPheThrGlyGlyLeuAspThrGlnIleGluHisIleLeu	426	
Db	1485	GCAGGGGTGTTAATGATGGTGTACCGGGAGGTCTCACAGACAGATTGGCATCATCTA	1544	
Qy	427	PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys	446	
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		ORGANISM		QY
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Qy	155	ArgGluglyLeuPheSerSerLysAlaTrpPheLeuGlnThrLeuIleAsnAla 174	ACCESSION AJ222981
Db	13901	AGGGAGCAACTTTCAAAGTCGAATTCTACTATGTTAGCTCACGAAATGTR 13960	VERSION GI:3790208
Qy	175	AlaLeuPheAlaLysAsnSerIleAlaThrIleCysThrAspLysSerIleVal 194	KEYWORDS delta6-acyl-lipid desaturase; dess6 gene.
Db	13961	GCTATTTTGCTCGAGCATGGCAAGACTATTTCGGGTTTG 14020	SOURCE Physcomitrella patens
Qy	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe 214	ORGANISM Physcomitrella patens
Db	14021	GCTTCAGCTTGATGGCTCTGTGTTCCAAACAGTGCGGATGGCTATCCATGATTG 14080	Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
Qy	215	LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTrpLeuPheGly 234	REFERENCE 1. Girke,T., Schmidt,H.-, Zahringer,U., Reski,R. and Heinz,E.
Db	14081	CTCCACAAATCAGGGTTCTGGGTTTAGTACAGGGTGTGGAGAAAGCTAACCTTCATCATGCT 14143	AUTHORS Identification of a novel delta 6-acyl-group desaturase by targeted
Qy	235	AsnCysValLeuGlyPheSerValSerTrpTrpIglnTrpLysHisAsnIleHisHisthr 254	TITLE gene disruption in Physcomitrella patens.
Db	14141	AACGCCGTTCTGGGTTAGTACAGGGTGTGGAGAAAGCTAACCTTCATCATGCT 14230	JOURNAL Plant J. 15 (1), 39-48 (1998)
Qy	255	AlaProAsnGluCysAspGluGlnTrpThrProLeuAspPheAspThrLeuPro 274	JOURNAL MEDLINE 98416756
Db	14201	GCTCCAAATGAAATGCGGATTCAGACTTACCAACCAATTGATGATACTCTCCCC 14260	PUBLMED 9744093
Qy	275	IleIleAlaIleTrpSerLysGluIleLeuValGluSerLysArgIleLeuArgVal 294	FEATURES 2 (bases 1 to 3518)
Db	14261	CTCATTCGCTGGAGCAAGGACATACTGGCACACAGTTGAGATAAGACATTCTGGCGAATC 14320	AUTHORS Girke,T.
Qy	295	LeuGlnTrpGlnHistyrMetIleLeuProLeuPheHemAlaArgTrpSerIleTrpThr 314	TITLE Direct Submission
Db	14321	CTCCAAATCACCACATCTGGTCTCATGGGCTCTGTTAGTTGGCTC 14380	JOURNAL Submitted (19-DEC-1997) Girke T., Institut fuer Allgemeine Botanik,
Qy	315	pheGlySerIleLeuPheGluIleLeuValAlaGlyLeuIleGlu 334	JOURNAL Universitaet Hamburg, Chhorststrasse 18, D-22609 Hamburg, GERMANY
Db	14381	TTTGGAACTGGAGATAACCTCTACAGGAAATGGCTCACCTGTGGAG 14440	LOCATION/QUALIFIERS
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 Job time : 5938 secs

RESULT 15
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 DEFINITION Sequence 5 from Patent WO0075341.
 ACCESSION AX058834
 VERSION AX058834 . 1 GI:12311154
 KEYWORDS
 SOURCE Ceratodon purpureus
 ORGANISM Ceratodon purpureus
 Heinz,E., Stymne,S., Lee,M., Girke,T., Sperling,P. and
 Zaehringer,U.
 REFERENCE 1 g(d) 6-acetylbenzene and g(d) 6-desaturase from ceratodon purpureus
 Authors: Zukaryota; Streptophytta; Embryophyta; Bryophyta;
 Bryopsida; Dicranidae; Dicranales; Bryophytina; Ceratodon.
 Title: Patent: WO 0075341-A 5 14-DEC-2000;
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 QY 251 IleHisIleHistAlaProAsnGluCysAspGluGlnItyrrhrProLeuAspGluAspIle 270

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	Query Match Length	DB ID	Description
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Scoring table:	IDENTITY_NUC				AX058840 Sequence
	Gapop 10.0 , Gapext 1.0				AU250735 Ceratodon
Searched:	3470272 seqs, 21671516995 residues				AX481617 Sequence
Total number of hits satisfying chosen parameters:	6940544				AX481946 Sequence
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Maximum DB seq length:	2000000000				Physcomit
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	Maximum Match 100%				AX481635 Sequence
	Listing first 45 summaries				AX481964 Sequence
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ALIGNMENTS

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DEFINITION	Sequence	from Patent	WO0075341.
ACCESSION	AX058830		
VERSION	AX058830.1	GI:12311150	
KEYWORDS			
SOURCE	Ceratodon purpureus		
ORGANISM	Ceratodon purpureus		
	Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;		
	Bryopsida; Dicranidae; Dicranaceae; Ditrichaceae; Ceratodon.		
REFERENCE			
AUTHORS	Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and Zaehringer, U.		
TITLE	Pred. No. is the number of results predicted by chance to have a g(d)-acetylenase and _g(d)-desaturase from ceratodon purpureus		

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RUN ON: June 18, 2004, 20:19:04 : Search time 7900 Seconds
          (without alignments)
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Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6940544

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a g(d)-acetylenase and _g(d)-desaturase from ceratodon purpureus

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		KEYWORDS	SOURCE	Ceratodon purpureus
		ORGANISM	Ceratodon purpureus	Bularyota; Viridiplantae; Streptophyta: Embryophyta; Bryophyta;
		REFERENCE	Heinz, B., Styrne, S., Lee, M., Girke, T., Sperling, P. and Zaehringen, U.	Dicranidae; Dicranales; Ditrichaceae; Ceratodone.
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VERSION	878	TATTCAACAGTGGGATGGTGTCTCACGATTCTACCATGAGTATTGAGACAGC	937	

	REFERENCE	2 (bases 1 to 2160)
	AUTHORS	Sperling, P.
	TITLE	Direct Submission
	JOURNAL	Submitted (28-OCT-1999) Sperling P., Dept. Plant Physiology, Institut fuer Allgemeine Botanik, Universitaet Hamburg, Ohnhorststrasse 18, D-22609 Hamburg, GERMANY
	FEATURES	Location/Qualifiers
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DEFINITION		Ceratodon purpureus mRNA for delta 6-fatty acid desaturase.
ACCESSION	AJ250735	AJ250735..1 GI:8670978
VERSION		Cytochrome b5; delta 6-fatty acid desaturase; desaturase.
KEYWORDS		Ceratodon purpureus Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Bryopsida; Dicranidae; Dicranales; Bryophyta; Bryophytaceae; Ceratodon.
ORGANISM		
REFERENCE		
AUTHORS		Sperling, P., Lee, M., Girke, T., Zahringer, U., Stymne, S. and Heinz, E.
TITLE		A bifunctional delta-fatty acyl acyl acyl esterase/desaturase from the moss Ceratodon purpureus. A new member of the cytochrome b5 superfamily
JOURNAL		Eur. J. Biochem. 267 (12), 3801-3811 (2000)
MEDLINE		20307617
PUBMED		10848999

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		Query Match 27.8%; Score 567.4; DB 6; Length 1578;			
		Best Local Similarity 66.3%; Pred. No. 2.5e-145;			
		Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;			
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DEFINITION		Phycomitrella patens		linear	
VERSION	AX481617	AX481617 GI:22316520		PAT 16-AUG-2002	
KEYWORDS		Phycomitrella patens			
SOURCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Funariidae; Funariales			
ORGANISM		Domergue, F., Zaehringer, U., Heinz, E., Renz, A. and Lerchl, J.			
REFERENCE	1	Method for producing polyunsaturated fatty acids, novel biosynthesis genes and novel plant expression constructs			
AUTHORS		Patent: WO 02057465-A 7 25-JUL-2002;			
TITLE				1018	
JOURNAL				1019 ATTGGGCCACCGTTGGAGAGCAAGGAAATTGGCTTCAATATCAGCACTACATG	1078

RESULT 8
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LOCUS AX069275 2012 bp DNA linear 25-JAN-2001

DEFINITION Sequence 1 from Patent WO0102591.

ACCESSION AX069275

VERSION GI:12579151

KEYWORDS Physcomitrella patens

SOURCE Physcomitrella patens

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

REFERENCE Heinz, E., Scheffler, J. and da costa e Silva, O.
Plants expressing γ (d)-desaturase genes and oils from these plants containing PUFAs and method for producing unsaturated fatty acids
Patent: WO 0102591-A 1 11-JAN-2001;
BASF AKTIENGESELLSCHAFT (DE)
Location/Qualifiers

JOURNAL 1. 2012

FEATURES source

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ORIGIN

Query Match 27.8%; Score 567.4; DB 6; Length 2012;
Best Local Similarity 66.3%; Pred. No. 2.7e-145;
Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

Qy 359 ACTTACTCTCTGGCCGATGTTGCCTTCAGCAAGGGCTGGAGACTGCTGGATGATCGTC 418
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REFERENCE	Girke, T., Schmidt, H., Zahzinger, U., Reski, R. and Heinz, E.			QY 779 CTCCTGTCACACAGTGTGGATGGCTTGCATCARCAAGCTCTTGGCT 638
AUTHORS	Identification of a novel delta 6-acyl-group desaturase by targeted			Db 1048 CTGTCGTTCAACAGTGCGGATGGCTATCCCATGATTTCACAAATCAGGTGTTGAG 1137
TITLE	gene disruption in Physcomitrella patens			QY 839 AACGGTACCGGAAACTCTTCTGGCTATTGTTCGGTAAATTGGCTTTAGT 898
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TITLE	Direct Submission			QY 1019 ATTITGGCACCCTGAGTGGCTTCAATATCAGCCTACATG 1078
JOURNAL	Submitted (19-DEC-1997) Girke T., Institut fuer Allgemeine Botanik, Universitaet Hamburg, Ohnstorstrasse 18, D-22609 Hamburg, GERMANY			Db 1288 ATACTGGCCACAGTGGAAATAAGACATCTGCGCATCTCTGCTGCTGCTTC 1347
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DEFINITION Sequence 25 from Patent WO02057465.

ACCESSION AX481635

VERSION AX481635.1 GI:22316538

KEYWORDS -unidentified

SOURCE ORGANISM unidentified unclassified.

REFERENCE 1. Domergue, F., Zaehringen,U., Heinz,E., Renz,A. and Lerch1, J.. Method for producing polyunsaturated fatty acids, novel biosynthesis genes and novel plant expression constructs Patent: WO 02057465-A 25 JUL-2002; BASF PLANT SCIENCE GMBH (DE)

AUTHORS

TITLE

JOURNAL

FEATURES

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ORIGIN

Query Match 27.8%; Score 567.4; DB 6; Length 15430;

Best Local Similarity 66.3%; Pred. No. 4.4e-145;

Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY 359 ACTTACTCTCTGGCCGATGTTGGCTTCACGACAGGCCGACTGCTGGGATGATCGTC 418

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Db 14462 TACTTTGGTTGTCGCGGACGGCTGCGTGGCTATCTTCTCCCTGGT---TGGAGGCCATTGTA 14518

QY 1259 TGATGGTAGCAACTGAGCTTGTGGGGATTGTTGGTTACGTTGAGT 1318

Db 14519 TGATGGGGTGACTIONGCTCATGTCGGCATGTCGGCTTGTGTTTGTACTTGTACCTAGC 14578

QY 1319 CACAATGGAAAGGGGTTTACAATGAAATCGAAGGACTTCGTGAGACGCCAGGTATTAC 1378

Db 14579 CACAATGGGATGGGTTTATATTCGTCATAAAGAATTCTGTGAGTGCACAGATGTATCC 14638

QY 1379 ACCCGTAACACCAAGGGCTGGTTCAACGATTGGTTCACTGGGGACTCGACACCCAG 1438

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DEFINITION AX481638 VERSION AX481638.1 GI:22316541 KEYWORDS unclassified SOURCE unclassified ORGANISM unclassified.

REFERENCE 1. Domergue, F., Zaetringger, U., Heinz, E., Renz, A. and Lerchl, J. Method for producing polyunsaturated fatty acids, novel biosynthesis genes and novel plant expression constructs. Patent: WO 02057465-A 28 25-JUL-2002; BASF PLANT SCIENCE GMBH (DE) Location/Qualifiers 1..-17752

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ORIGIN Query Match 27.8%; Score 567.4; DB 6; Length 17752;
 Best Local Similarity 66.3%; Pred. No. 4.5e-145;
 Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

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Db 13742 AGTACTTATTGGGCCGGATGGCACAGACGTTTGCBAACATCCACCTGCCGA 538

Db 13801 TGAGGGCAACTCATGACTACTACATTGGAGACCTTGCTTAGGGAGAGGCCCTGTGTA 598

Db 13802 TGAAAATTCTCAAGACTTTACATTGGTAGCTGGAGAGGGTGGAGACTCCAGAG 13861

Db 13862 CTGCTGAAGATTCCGAGAAATGAGAGCTCTTTCCCTGAGGGACAACTTCAAAGT 13921

Db 13982 GCAATAATATGGTCTCAGACTCTGATTAATGCAAGCTCTCTGCTGAGCTTCAAGACT 718

Db 13922 TCGAAATTGTACTATGTTATGAAAGCTGCTCAAGAAATGTTGCTGCGAGCATT 13981

Db 13982 GCAAGGCTGGTTCTGCTCAGACTCTGCTCTTGTGCTGAGCTTCAAGACT 778

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RESULT 13

AX481967 AX481967 17752 bp DNA linear PAT 16-AUG-2002
DEFINITION Sequence 28 from Patent WO20057464.
ACCESSION AX481967
VERSION AX481967.1 GI:22316695
KEYWORDS unclassified
SOURCE unclassified
ORGANISM unclassified

REFERENCE Heinz,E., Duwening,E., Bischoff,F., Drexler,H. and Lerchl,J.S.
AUTHORS Method For the expression of biosynthetic genes in plant seeds
TITLE using novel multiple expression constructs
Patent: WO 02057464-A 28 25-JUL-2002;
BASF PLANT SCIENCE GMBH (DE)

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ORIGIN

Query	Match	Score	DB	Length
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Matches	8333;	Conservative	0;	Mismatches
		Indels	3;	Gaps

Y 359 ACTTA

Db 13622 ACAC

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Db 13682 AAAAACAGGTGTATGATGTTCAATTTGGGAGGATCAGTTATT 13741

Y 479 AGCACCTACTTTGGCGGGATGGCACAGACGTTTCGOAACATCCATCCACCTGGCGCA 538

Db 13742 AGTACTTATTGGACAGATGTTCTCTAGTTTATGCACTCTACA 13801

Y 539 TGGAACTCAATGACTACTACATGGAGACCCCTGCTAGGGAAAGAGCCCTTGATGAA 598

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Y 599 TTGCTTAAGACTACAGAGATATGAGAGCCGAGTTGTAGAGAAGGGCTTTCAAGAGT 658

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RESULT 14
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 DEFINITION Sequence 5 from Patent WO0075341.
 VERSION AX058834
 ACCESSION AX058834.1 GI:12311154
 KEYWORDS Ceratodon purpureus
 SOURCE Ceratodon; Viridiplantae; Streptophyta; Bryophyta;
 ORGANISM Eukaryota; Dicranidae; Dicranaceae; Ceratodon.

REFERENCE 1
 AUTHORS Heinz, E., Stymne, S., Lee, M., Girke, T., Sperling, P. and Zaehringer, U.
 TITLE g(d) 6-acetyl enase and g(d) 6-desaturase from ceratodon purpureus
 JOURNAL Patent: WO 0075341-A 7 14-DEC-2000;
 FEATURES BASEF AKTIENGESELLSCHAFT (DE)
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Query Match 12.5%; Score 254.6; DB 6; Length 514;
 Best Local Similarity 69.6%; Pred. No. 7.2e-59;
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QY 985 TGATACTCTCCCACATTGCCTGAGCAAGAAATTGGCCACCGTTGAGACCAAGAG 1044
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QY 1045 AATTGGGAGTTGGACTTTGAAAGTTGGCTCTCAGCTCAATCCTGATTGAGCACGACAT 1104
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QY 1105 GTACAGTTGGACTTTGAAAGTTGGCTCTCAGCTCAATCCTGATTGAGCACGACAT 1105
 Db 181 GCGGAGTTGGCTATTGGCTTCACTGGCCGAGTGGCTTGGCGA 240

QY 1165 GGAGTTGATGAGAAAGGAAACAGTTGGCTCTCAGCTGGCTGGCTGGCGTT 1224
 Db 241 GAGCTTTGGAGAGGGAAACGATGGCTTGCACATGGCTTGGCTGGCGTT 300

QY 1225 CCATATTGCGGGTTGGGATTCAGTTGAGGACTACATGGCTGGCTGGCGTT 1284
 Db 301 TTATCTGCTCCCGG--ATGGAAACCAGTTGCTGGCTGGGATGGCTCATGTC 357

QY 1285 CGGTTTGGACTTTGGAGTTGCTGGCTGGCTGGCGTT 1344
 Db 358 TGGTTTCCGTGGCTGGGATACGTTGCTGGCTGGCGTT 417

Qy 1345 ATCGAAGGACTTCGTGAGGCCAGGTTATTACCAACCCGTAACACCAAGCGAGGCTGGTT 1404
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Qy 1405 CAACGATGGTTCACTGGGGACTCGACACCCAGAT 1441
Db 478 TAATGATGGTTCACCGGAGGTCTAACAGACAGAT 514

Search completed: June 19, 2004, 01:08:04
Job time : 7910 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2004, 20:15:54 ; Search time 818 Seconds
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10594.528 Million cell updates/sec

Title: US-09-980-468-1

Perfect score: 2040
Sequence: 1 ctccaggaggctcgatgtaa.....aaaaaaa.....aaaaaaa 2040

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

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2: geneseqn1990s;*
3: geneseqn2000s;*
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9: geneseqn2003cs;*
10: geneseqn2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1456.4	71.4	1467	4	AAF25730		Aaf25730 C. purpur
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5	567.4	27.8	1578	6	ABQ76782		Abq76782 P. patens
6	567.4	27.8	2012	4	AAF26040		Aaf26040 P. patens
7	567.4	27.8	2012	7	ABX13450		Abx13450 P. patens
8	567.4	27.8	15430	6	ABV74274		Abv74274 Plant spe
9	567.4	27.8	15430	6	ABQ76796		Abq76796 PB-DHGLA
10	567.4	27.8	17752	6	ABV74275		Abv74275 Plant spe
11	567.4	27.8	17752	6	ABQ76797		Abq76797 PBARAL en
12	518.4	25.4	520	4	AAF25731		Aaf25731 C. purpur
13	254.6	12.5	514	4	AAF25732		Aaf25732 C. purpur
14	153	7.5	1617	2	AAV63624		Aav63624 cDNA enco
15	153	7.5	1617	2	AAX00889		Aax00889 Mortierel
16	153	7.5	1617	3	AAA09430		Aaa09430 M. alpina
17	152.2	7.5	1374	5	AAF25234		Aaf25234 Nucleotid
18	150.6	7.4	1374	3	AAZ47129		Aaz47129 Fungal de
C 19	137.6	6.7	451	4	AAH56929		Aah56929 P. patens
C 20	137.6	6.7	451	4	AAH56909		Aah56909 P. patens
C 21	137.6	6.7	451	5	AAH50922		Aah50922 Lipid mod
22	114	5.6	1380	6	AAD35090		Aad35090 Pythium i
23	103.4	5.1	1471	3	AAD01349		Aad01349 Florida b

ALIGNMENTS

RESULT 1
ID AAF25729 standard; DNA; 2040 BP.
XX AAF25729;
XX AC
XX DT 06-APR-2001 (first entry)
XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 1.
XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
KW cosmetic; ds.
XX OS Ceratodon purpureus.
XX FH Key
FT FT 176. .1627
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FT FT /product= "delta6-acetylenase/delta6-desaturase"
XX PN WO200075341-A1.
XX PD 14-DEC-2000.
XX PP 07-JUN-2000; 2000WO-EP005274.
XX PR 07-JUN-1999;
PR 22-DEC-1999;
XX XX 'BASF I) BASF AG.
XX DR 2001-112150/12.
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U,
DR P-PSDB; AAB46435.

XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for
PT producing plant oils with increased content of unsaturated fatty acids.
XX PS Claim 1a; Page 41-44; 69pp; German.
XX CC This invention describes a novel isolated nucleic acid (I) encoding
CC polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase
CC activity. The invention also describes (a) amino acid sequences encoded
CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
CC

more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (III), resulting in oils with increased content of saturated fatty acids.

XX Sequence 2040 BP; 528 A; 450 C; 505 G; 557 T; 0 U; 0 Other;

Query Match 100.0%; Score 2040; DB 4; Length 2040;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	Qy	1 CTCAGGGAGGTCTCACTTGTGAGCACGGCTCTGAATCCTTGAGCTGTGAGGGT 60	Db	Qy	1 CTCAGGGAGGTCTCACTTGTGAGCACGGCTCTGAATCCTTGAGCTGTGAGGGT 60	Db	Qy	1 CGGGACTGTGGGATGGTGAAGGAGTGTGGATCAGGAGTCAGCTTAGTTIC 61	Db	Qy	1 CGGGACTGTGGGATGGTGAAGGAGTGTGGATCAGGAGTCAGCTTAGTTIC 61	Db	Qy	121 TCAGGGTCTGATCACGGTTATTCTGAAAAAAGGCTCGGTCTGTGAGCAGTTGCAC 120	Db	Qy	121 TCAGGGTCTGATCACGGTTATTCTGAAAAAAGGCTCGGTCTGTGAGCAGTTGCAC 120	Db	Qy	181 CCTCGTTACCGACTTCTGAACCTTCTGAAACTGGCTCTGGTCAAGGGTTCAC 180	Db	Qy	181 CCTCGTTACCGACTTCTGAACCTTCTGAAACTGGCTCTGGTCAAGGGTTCAC 180	Db	Qy	241 CCATAGCTATGCTGGAAACTGGCCCTACTTGGCAGCTGGCTCTGGTCAAGGGT 240	Db	Qy	241 CCATAGCTATGCTGGAAACTGGCCCTACTTGGCAGCTGGCTCTGGTCAAGGGT 240	Db	Qy	301 AGGTAAAAACTGCGGACAGACACTGAGACAGAGTCGGGACAAAAGGCTGTACAC 360	Db	Qy	301 AGGTAAAAACTGCGGACAGACACTGAGACAGAGTCGGGACAAAAGGCTGTACAC 360	Db	Qy	361 TTACTCTCGCGATGGCTCTCACGACAGGCTGGAGACTCTGGCTCTGGCTCA 300	Db	Qy	361 TTACTCTCGCGATGGCTCTCACGACAGGCTGGAGACTCTGGCTCTGGCTCA 300	Db	Qy	421 AGAGAACGGTGTATGATAATTAGCCGTTGGGACGACCACCCCTGGAGCTTAATTAG 480	Db	Qy	421 AGAGAACGGTGTATGATAATTAGCCGTTGGGACGACCACCCCTGGAGCTTAATTAG 480	Db	Qy	481 CACCTDACTTTGGCGGAGATGGCAACAGACGTTTGCACACATTCCACCTGGCGCATG 540	Db	Qy	481 CACCTDACTTTGGCGGAGATGGCAACAGACGTTTGCACACATTCCACCTGGCGCATG 540	Db	Qy	541 GAAGCAACTCAATGAACTACTACATTGAGAACGGCTTGTAGAGAACGGCTTGTAGAAT 600	Db	Qy	541 GAAGCAACTCAATGAACTACTACATTGAGAACGGCTTGTAGAGAACGGCTTGTAGAAT 600	Db	Qy	601 GCTTAAAGGACTACAGAGATAATGAGAACGGCTTGTAGAGAACGGCTTGTAGAAT 660	Db	Qy	601 GCTTAAAGGACTACAGAGATAATGAGAACGGCTTGTAGAGAACGGCTTGTAGAAT 660	Db	Qy	661 CAAGGCCCTGGTTCTGTTCAAGACTCTGATTAATGCAAGCTCTTCAAGAGTTC 720	Db	Qy	661 CAAGGCCCTGGTTCTGTTCAAGACTCTGATTAATGCAAGCTCTTCAAGAGTTC 720	Db	Qy	721 GACTATCTGTTACGACAAGAGTACTGGCTATTGTGCTGTCAAGCCAGTTGATGGGTCT 780	Db	Qy	721 GACTATCTGTTACGACAAGAGTACTGGCTATTGTGCTGTCAAGCCAGTTGATGGGTCT 780	Db	Qy	781 CTTCGTCCAAACAGTGTGGATGGCTGCCATGCTTCCATCAACAGGTCTTGAGAA 840	Db	Qy	781 CTTCGTCCAAACAGTGTGGATGGCTGCCATGCTTCCATCAACAGGTCTTGAGAA 840	Db	Qy	841 CGGTACCGGAAACTCCCTCTGGCTTATTGGCTGGATGGCTGCCATGATTTCCCTCATG 900	Db	Qy	841 CGGTACCGGAAACTCCCTCTGGCTTATTGGCTGGATGGCTGCCATGATTTCCCTCATG 900	Db	Qy	901 ATCATGGTGGAGGACACATTCACTGCTCCGAATTGAGTGGCTTGTGAGGARCA 960	Db	Qy	901 ATCATGGTGGAGGACACATTCACTGCTCCGAATTGAGTGGCTTGTGAGGARCA 960	Db	Qy	961 GTACACACCTCTAGACGAAGACATGATACTTCCCATTGGCTGGAGCAAGGAAT 1020	Db	Qy	961 GTACACACCTCTAGACGAAGACATGATACTTCCCATTGGCTGGAGCAAGGAAT 1020	Db	Qy	1021 TTGGCCACCGTTGAGGAAAGACAATTTCGAGCTACATGATGATGAT 1080	Db	Qy	1021 TTGGCCACCGTTGAGGAAAGACAATTTCGAGCTACATGATGATGAT 1080	Db	Qy	1081 TCTGCCTCTATTGTTCATGGCCGGTACAGTTGGSACTTTGGAAATTGGCTCTCACATT 1140	Db	Qy	1081 TCTGCCTCTATTGTTCATGGCCGGTACAGTTGGSACTTTGGAAATTGGCTCTCACATT 1140	Db	Qy	1141 CAATCCTGATTTGAGCACGACCAAGGGATTGATAGAAAGGAAACAGTTGCTTTCACTA 1200	Db	Qy	1141 CAATCCTGATTTGAGCACGACCAAGGGATTGATAGAAAGGAAACAGTTGCTTTCACTA 1200	Db	Qy	1201 CGCCCTGGTTCACTGGCTGGCTGCTTAAGGCTCTTGGCTG 1260	Db	Qy	1201 CGCCCTGGTTCACTGGCTGGCTGCTTAAGGCTCTTGGCTG 1260	Db	Qy	1261 GATGGTAGCAACTGAGCTGGCTGGCGGTTGGGATTCAGTTGAGTGAAGTCA 1320	Db	Qy	1261 GATGGTAGCAACTGAGCTGGCTGGCGGTTGGGATTCAGTTGAGTGAAGTCA 1320	Db	Qy	1321 CAATGGAAAGGAGGGTTACAATGAATCGAAGGACTTCGGTGAAGGCCAGGT 1380	Db	Qy	1321 CAATGGAAAGGAGGGTTACAATGAATCGAAGGACTTCGGTGAAGGCCAGGT 1380	Db	Qy	1381 CGTAACACCAAGCGAGGTCTCAACGATGGTTCACTGGGGACTCGACACCCAGAT 1440	Db	Qy	1381 CGTAACACCAAGCGAGGTCTCAACGATGGTTCACTGGGGACTCGACACCCAGAT 1440	Db	Qy	1441 TGAGCATCACCTGTTCCAAACTACGATGGCTGGTCAACGATGGCTCAGGT 1500	Db	Qy	1441 TGAGCATCACCTGTTCCAAACTACGATGGCTGGTCAACGATGGCTCAGGT 1500	Db	Qy	1501 CGAGGCTCTTTGCAAGAACGCAOGGCCCTGGCTCGTTGGCCTC 1560	Db	Qy	1501 CGAGGCTCTTTGCAAGAACGCAOGGCCCTGGCTCGTTGGCCTC 1560	Db	Qy	1561 TGTGGGGTTGTGAAGGGCTCAAGGAATTGGTGTAGAAGGCTACCTCAAATGTT 1680	Db	Qy	1561 TGTGGGGTTGTGAAGGGCTCAAGGAATTGGTGTAGAAGGCTACCTCAAATGTT 1680	Db	Qy	1621 TCACTAAGAAATCGTCACTTCTGCTGGCTACCTCAAATGTTGGCTTCAAGGC 1620	Db	Qy	1621 TCACTAAGAAATCGTCACTTCTGCTGGCTACCTCAAATGTTGGCTTCAAGGC 1620	Db	Qy	1681 CGGGAGGAGGTGCTGGCAACTGTTCAACCGGAGGGCTCAACTGAAATCCAT 1740	Db	Qy	1681 CGGGAGGAGGTGCTGGCAACTGTTCAACCGGAGGGCTCAACTGAAATCCAT 1740	Db	Qy	1741 TCCAGAAATTACCATCTCTAGTAAATCTTCTCTTACAGGTGGATATGAAACTT 1800	Db	Qy	1741 TCCAGAAATTACCATCTCTAGTAAATCTTCTCTTACAGGTGGATATGAAACTT 1800	Db	Qy	1801 TTITGATGCAACAGTGTGGCTTCAATTGAGACATTTGAGATAATTTCGAGTGT 1860	Db	Qy	1801 TTITGATGCAACAGTGTGGCTTCAATTGAGACATTTGAGATAATTTCGAGTGT 1860	Db	Qy	1861 TTIAATTCAAGGGGGCATACGTACTAGTCCATATCGCGAGGTGTGGCTTACATTATA 1920	Db
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SO	Sequence	1467 BP; 356 A; 349 C; 379 G; 383 T; 0 U; 0 Other;
b	1861	TCTATTAGGGGCAATACGTACTAGTCCCATATCGCGGTTGCCGAGAGTTACATTTA 1920
b	1921	GGGGCAGACAGGAGTAGATCTAGTAAATTCTATTTCCGCAATGTAATACTCTTGAA 1980
b	2921	GGGGCAGACAGGAGTAGATCTAGTAAATTCTATTTCCGCAATGTAATACTCTTGAA 1980
b	1981	TATATAACCSTTATCTTTCCTAAAGAAAAAAAGAAAAA 2040
b	1981	TATATAACCCTTATCTTTCCTAAAGAAAAAAAGAAAAA 2040
b	171	CAAAATGGCCCTCGTACCCGACTTTCTGAACCTTCTGGGCACGACATGGCAAGTACA 230
b	5	CCAARATGGCCCTCGTACCCGACTTTCTGGGCACGACATGGCAAGTACA 64
b	231	GCGTGTACACCCATAAGCTATGGAAACTATGGCCTACTTTGAAGGCACGGCAAAGGG 290
b	65	GCGTGTACACCCATAAGCTATGGAAACTATGGCCTACTTTGAAGGCACGGCAAAGGG 124
b	292	TTCTGCTCAAGGTTAAACTGGGACAGACACTGAGAACAGAGATGGGTGGAGACTGGGCTAAAGAAA 350
b	125	TTCTGCTCAAGGTTAAACTGGGACAGACACTGAGAACAGAGATGGGTGGAGACTGGGCTAAAGAAA 184
b	351	AGCCAGGGCACTTACTCTCGCGGATGTTGCTTCACGACAGGGACTGGCTGGA 410
b	185	AGCCAGGGCACTTACTCTCGCGGATGTTGCTTCACGACAGGGACTGGCTGGA 244
b	411	TGATCGTCAAAAGGAAAGGTGTATGATATTAGCCGGATGGCACCCCTGGAGGAA 470
b	245	TGATCGTCAAAAGGAAAGGTGTATGATATTAGCCGGATGGCACCCCTGGAGGAA 304
b	471	CGGTAAATTAGCACTACTTGGCGGATGGCACAGACGTTTCGCAACATTCATCCAC 530
b	305	CGGTAAATTAGCACTACTTGGCGGATGGCACAGACGTTTCGCAACATTCATCCAC 364
b	531	CTGCCGCGATGGCAAGGCAACTCAATGACTACTACATTGGAGACCTGGAGGCCCC 590
b	365	CTGCCSCTGGAAACTCAATGACTACATTGGAGACCTGGACTACATGGAGGCCCC 424
b	591	TGATGAATTGGCTTAAGGACTACAGAGATATGGAGAGCCGAGTTAGAGAAGGGCTTT 650
b	425	TGATGAATTGGCTTAAGGACTACAGAGATATGGAGAGCCGAGTTAGAGAAGGGCTTT 484
b	485	TCAAGAGTTCCAAAGGCCCTGTTCAAGACTCTGATTAATGAGGGCTT 544
b	711	CGAGCATTGGCACTATCTGTTACGACAGGTTCTCAGACTCTGATTAATGAGGGCTTT 710
b	545	CGAGCATTGGCACTATCTGTTACGACAGGTTCTCAGACTCTGATTAATGAGGGCTTT 604
b	771	TGATGGCTCTTCGTCACAGTGGGATGGCTTGGCCATGATTGCTTCAGCCAGTT 830
b	605	TGATGGCTCTTCGTCACAGTGGGATGGCTTGGCCATGATTGCTTCAGCCAGTT 664
b	665	TCTTGGAGAACGGTACCCGTACCGGAACACTCCCTCTTGGCTATTGTTGGCTTG 724
b	891	GCTTITAGTTGTTATCATGGTCCAAACAGTGGGTTGGCTTGGCCATGATTGCTTCAGGGCTTG 950
b	725	GCTTITAGTTGTTATCATGGTCCAAACAGTGGGTTGGCTTGGCCATGATTGCTTCAGGGCTTG 784
b	951	GGGACGAACTACACCTCTAGAGGAGCATGGAAACTCTCCCACATGGCTTGAA 1010
b	785	GGGACGAACTACACCTCTAGACGAAAGACATTGATACTCTCCCACATGGCTTGAA 844
b	1011	GCAAGGAAATTGGCCACCGTTGAGGCAAGAGAAATTGGGAGTGGCTTCAATATCAGC 1070
b	845	GCAAGGAAATTGGCCACCGTTGAGGCAAGAGAAATTGGGAGTGGCTTCAATATCAGC 904
b	1071	ACTACATGATTGGCTCTATGGTTCATGGCCCGTACAGTTGGAAAGTTTGCG 1130
b	905	ACTACATGATTGGCTCTATGGTTCATGGCCCGTACAGTTGGAAAGTTTGCG 964
b	1131	TCTTCACATTCAATCCTGATTGGCAACGGGAACTGGCTTCAATATCAGC 1190
b	965	TCTTCACATTCAATCCTGATTGGCAACGGGAACTGGCTTCAATATCAGC 1024

QY	1191	CTTTCACTACGCCCGGTTCACTGGGTCCATATTGGCGGGTTCGCTTAAGC	1250	XX	Claim 1a; Page 54-57; 69pp; German.
Db	1025	CTTTCACTACGCCCGGTTCACTGGGTCCATATTGGCGGGTTCGCTTAAGC	1084	CC	This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids
QY	1251	CTCTTGGGGATGCTAGAACACTGGCTTGTGGATTCGGATGGTGTGTTA	1310	CC	XX
Db	1085	CTCTTGGGGATGCTAGAACACTGGCTTGTGGATTCGGATGGTGTGTTA	1144	CC	CC
QY	1311	CGTTGAGTCACAATGGAAAGGAGGTTAACATGAATCGAAGGACTTCG	1370	CC	CC
Db	1145	CGTTGAGTCACAATGGAAAGGAGGTTAACATGAATCGAAGGACTTCG	1204	CC	CC
QY	1371	TTATTACCAACCCGTAAACCCAAGGAGCTGGTTCAACGATTGGGACTCG	1430	CC	CC
Db	1205	TTATTACCAACCCGTAAACCCAAGGAGGTTAACATGAATCGAAGGACTCG	1264	CC	CC
QY	1431	ACACCCAGATTGAGCATCACCTGTTCCAACAATGCCCAAGGACATCG	1490	CC	CC
Db	1265	ACACCCAGATTGAGCATCACCTGTTCCAACAATGCCCAAGGACATCG	1324	CC	CC
QY	1491	CACCTCAGGGTCGAGGACTCTTGCAGAACGGCCTCGAGAGTACGATA	1550	CC	CC
Db	1325	CACCTCAGGTGAGGCTCTNGCAAGGAGCACGGCCCTCGAGTAGTCG	1384	CC	CC
QY	1551	TGGGTGCCCTCTGTCGGGTTGAAGGAAATTGCTGATGAAAGCTCAATTC	1610	XX	Sequence 2160 BP; 509 A; 481 C; 556 G; 614 T; 0 U; 0 Other;
Db	1385	TGGTGCCTCTGTCGGGTTGAAGGCGCTCAAGGAAATTGCTGATGAAAGCTCAATTC	1444	XX	Query Match 32.8%; Score 670; DB 4; Length 2160;
QY	1611	GGCTTCACGCTCACTAAG 1628	XX	Best Local Similarity 69.8%; Pred. No. 1.7e-155;	
Db	1445	GGCTTCACGCTCACTAAG 1462	XX	Mismatches 0; Indels 3; Gaps 1;	
RESULT 3					
ID	AAF25734	standard; DNA; 2160 BP.	XX	Matches 920; Conservative 0; Mismatches 395; Indels 3; Gaps 1;	
XX	AAF25734		Db	304 TAAMACTGGGGACAGACACTGAGACAGGATCGGTGATGTCAGGTAAGA	
AC	AAF25734;		Db	398 TCAATGGGTTGGCGAGCCCCATGGCACGATATGCCCGAGGGTACTTA	
XX	06-APR-2001 (First entry)		QY	364 CTCTCYGGCGATGTTGCTTCTACAGACAGGCTGGAGACTGCTGTAAGA	
DE	C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 11.		Db	458 CAGGCTGAAGGATGTAGTGTAGTGTAGCTGAGCACCTGAGCTAACACAC	
XX	DT		QY	484 CTACTTGGGGATATTAGCCGTTTGCAGACGCTTGCACATCCACCTGCCGATGAA	
XX	XX		Db	578 CTACCTGGACGAGACGCCACAGATGTTCTACTTCCACGATCCACCTCATGGAA	
DE	purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 11.		QY	544 GCAACTCAATGACTACTACATTGGAGACCTGCTAGGGAAAGGCCCTTGATGATTGCT	
XX	XX		Db	638 GATTCTCAGAAATTCTACATGGGAAACCTGTTAGGGAGGCCGACTTTGGAGCTGCT	
DE	Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid; transgenic plant; plant oil; triglyceride; nutrition; animal feed; cosmetic; ds.		QY	604 TAAAGACTACAGAGATATGAGAGGCCGAGTTGTTAGAGAAGGGCTTTCAAGAGTTCCAA	
XX	OS		Db	698 GAGGGAGTACAGAGAGTTGAGAGGCCCTTTCTAGAGAACAGGTTCCAA	
XX	Key	Location/Qualifiers	QY	664 GGCTCTGGTCCCTGCTCTGACTCTGATGGGCTATTGGCAGATTGGCAC	
FT	159..1721		Db	758 ATCCTACTACCTTTCAAGACTCTAAATGTTCCATTGTCAGGATTGGCAT	
FT	/tag= a		QY	724 TATCTGTTACGACAAGAGTTACTGGCTATGCTGCTAGCCAGTTGATGGGTCTCTT	
FT	/product= "delta6-acetylenase/delta6-desaturase"		Db	813 ATCAGTCTGTAAGCTTACAGCTTACGGATGGCTTCTGTTATGAGGCTTGTGTT	
XX	PN WO2000075341-A1.		QY	784 CGTCCAACAGTGTGGATGGCTTCCCTCATCAACAGGTCTTGGAGAACCG	
XX	PD 14-DEC-2000.		Db	878 TATCAACAGTGTGGATGGCTTCTACGATTCTACACCTGAGCTTGTGACACG	
PP	07-JUN-2000; 2000WO-EPO05274.		QY	937 PA (BADI) BASF AG.	
XX	PR 07-JUN-1999; 99DE-01025718.		Db	938 CTGGCTCAATGAGCTTGGCTATGGGGATGGCTAGTGTGCTC	
PR	22-DEC-1999; 99DE-01062409.		QY	964 ATGGTGGGAACTCCTTGGCTATTGGCGAATTGGCTGTTAGTGTATC	
XX	PA (BADI) BASF AG.		Db	998 GTGGTGGAAAGCCAACCTGCATGCTGCTC	
PI	Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringen U;		QY	999 GTGGTGGAAAGCCAACCTGCATGCTGCTC	
XX	WPI; 2001-112150/12.		Db	1057 Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.	
DR	P-PSDB; AAB46440.		QY	1023 PT	
XX	PT		Db		
PT	964 ACACCTCTAGAGAACATTGATACTCTCCCATTGCTGGCAAGGAAATT	1023	QY		

Db 1058 CACCCGATTGATGGATAATTGATACTCTCCCCATCATTCATTGCTTGGAGTAAGATCTCTT 1117
 Qy 1024 GGCCACCGTTGAGAGATAAGAGATAATTGGCAGTGCTTCAATACTGGCACTACATGATTCT 1083
 Db 1118 GGCCACTGTTGAGAGCAAGACCATGTTGGAGTTCTTCAAGTACAGCACCTATTCTT 1177
 Qy 1084 GCCTCTTATGTTGAGCTTACAGTTGGACTTTGGAAAGTTGCTCTCACATTCAA 1143
 Db 1178 GGTTCTTTGAGCTTGCCTGGGAGTTGGCTATTGGAGCCCTTCACTCTCAG 1237
 Qy 1144 TCCTGATTGAGCACGACCAAGGAACATAGAGAAGGGATTCACTACAGC 1203
 Db 1238 GCGCGAGTGCACCTTGGGAGAACGATGGGAACGGGAACCTGGCTTCACTACAT 1297
 Qy 1204 CTGGTTCACTTGGGTGCGTTTCATATTGGCGGGTGTGCTTAAGCCTCTGGGTGGAT 1263
 Db 1298 TTGGTTTAATAGTGTGCGTTTTATCTGGCTCCCGG---ATGGAACCACTGGTGTATGGAT 1354
 Qy 1264 GGTAGCAACTGAGCTTGTGGCTGGTTACGTGAGTCACA 1323
 Db 1355 GGTGGTCAGGGAGCTATGTCGGTTTCCTGTGGGATACGTCACTGTCACA 1414
 Qy 1324 TGGAAAGGAGGTTTACAATGAATCGAAGGACTTGTGAGAGGCCAGGTTAACCCCG 1383
 Db 1415 TGGAAATGGAGGTGTACAATACGTCAAAAGGACTTCGTGAATGCCATCGACTCG 1474
 Qy 1384 TAACACCAAGCAGGGCTGGTTCAACGATGGTCACTGGGGACTCGACACCCAGATTGA 1443
 Db 1475 CGACATCAAGGAGGGTGTAAATGATTGGTCAACGGAGGTCTCAACAGMAGATTGA 1534
 Qy 1444 GCATCACCTGGTTCCAACAAATGCCACGGCAACTACCCAAAGATCGCACCTCAGGTGCA 1503
 Db 1535 GCATCATCTTTCACGATGCCACGGCACACTTAAATAAAATTCTCCCTCACGTGGA 1594
 Qy 1504 GGCTCTTCAAGAACGGACCGGCTCGAGTAGCTCGATAATGCTCCGGTGTGTTCTCTCTCGT 1563
 Db 1595 GACTTTGCAAGAACGGACATGGGATGGCTCGAGACTGGCATGGCTTCGGCACTTA 1654
 Qy 1564 CGCGTTTGTGAAGGGGCTCAAGGAATTGCGTGAATTCGGCTTCACGCT 1621
 Db 1655 CGGGTTTTGAAAAACACTTAAGGACGTTGCGATGCTGTTCAACACCAGCTTGT 1712
 Qy 4 RESULT 4
 Db ABV74260
 ID ABV74260 standard; cDNA; 1578 BP.
 XX ABV74260;
 AC
 XX DT 28-MAR-2003 (First entry)
 XX DE Physcomitrella patens desaturase encoding cDNA SEQ ID NO 7.
 XX Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
 KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
 KW gene; ss.
 XX OS Physcomitrella patens.
 XX FT Location/Qualifiers
 FT 1.: 1578
 FT /tag= a
 FT /product= "desaturase"
 XX PN DE102337-A1.
 XX PD 25-JUL-2002.
 XX PR 19-JAN-2001; 2001DE-01002337.
 XX PR 19-JAN-2001; 2001DE-01002337.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX PI Lerchl J, Renz A, Heinz E, Domerque F, Zaehringer U;
 XX DR WPI: 2002-644810/70.
 XX P-PSDB; ABB98277.
 XX PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in
 PT animal or human nutrition, by transforming organism with desaturase gene
 PT from Phaeodactylum tricornutum.
 XX PS Example 16; Page 60-63; 182pp; German.
 XX
 The invention relates to preparing (M1) fatty acid esters (I) with an
 CC increased content of polyunsaturated fatty acids (II) with at least two
 CC double bonds by introducing into a (I)-producing organism a specific
 CC nucleic acid (A). (M1) is useful for preparing ester containing
 CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
 CC produced by (M1) are used in animal and human nutrition, cosmetics and
 CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
 CC the blood and to protect against heart disease. Cells that express (A)
 CC are also used to identify (ant)agonists of desaturases, e.g. for
 CC modulating the yield and rate of production of particular fine chemicals
 CC in microorganisms (claimed). Also (A) and derived proteins can be used as
 CC markers of specific genomic regions and in evolutionary/protein
 CC structural studies. (M1) is suitable for large scale production (no known
 CC bioengineering method can produce (II) on a useful scale). The present
 CC sequence is that of a Physcomitrella patens desaturase encoding cDNA used
 CC as the (A) component of the invention in producing transgenic (I)-
 CC producing organisms
 XX SQ Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;
 Query Match 27.8%; Score 567.4; DB 6;
 Best Local Similarity 66.3%; Pred. No. 3.8e-130;
 Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
 Qy 359 ACTTACTCTGGCCGATGTTGCTCTCACGACAGSSCTGGAGACTGCTGGATGATCGTC 418
 Db 310 ACACACCCCTATCAGAAGTAGGTACACACAGGGCAAGGGATTTGGATGGTGTGTA 369
 Qy 419 AAAGAGAAGGTGTATGATAATTAGCCTGTTGGGACGACCCCTGAGGGACGGTAATT 478
 Db 370 AAAAACAGGTGTATGATGTTCCAAATTGGGGAGGATCCGGACGATCCGGAGATTATT 429
 Qy 479 AGCACCTACTTTGGGCGGGATGGCACAGACGTTTGGCACATCCATCCACCTGGCGCA 538
 Db 430 AGTACTTATTGGACCTTACATGGTGTCTAGTTCTATGCAGTTCTACA 489
 Qy 539 TGGAAAGCAACTCAATGACTACATGGAGACCTTGCTAGGGAAAGAGCCCTTGATGAA 598
 Db 490 TGAAAATTCTCAGACTTTACATTGGTACGTGGAGGGTGGAGGGAGCTCCAGAG 549
 Qy 599 TTGCTTAAGGACTACAGAGATATGAGGGCTTGTAGAGAAGGGCTTTCAAGAGT 658
 Db 550 CTGCTGAAGGATTCCGAGAAATGAGACGCTTGTGTTCAACACCAGCTTGT 609
 Qy 659 TCAAAGGCCGGTTCTGCTTCAAGACTCTGATAATGGCAGCTCTCTGCTGGGAGGATT 718
 Db 610 TCGAAATTGTACTATGTTGAGCTACAGGAATGTGCTATTGCTGCGAGCATT 669
 Qy 719 GCGACTATCTGTTACGACAAGAGTACT3GGCTATTGCTGTGCTGAGCTTGGGT 778
 Db 670 GCGAAATAATGTTGGAGCAAGACTATTTCAGGGTGTCTGAGCTTGTATGATGGCT 729
 Qy 779 CTCTTGTGTCACAGTGTTACGACAAGAGTACT3GGCTATTGCTGTGCTGAGCTTGGGT 838
 Db 730 CTGCTGTTCCACAGTGGCTATTGCTGGCAATTCGCTGCTGGCTTAGT 789
 Qy 839 AACCGTACCGGAACACTCTCTTCTGGCTATTGCTGGCAATTCGCTGCTGGCTTAGT 898
 Db 790 ACACGCTGGGTTAATGAAGTTGCTGGGATGGCTGATGGCTGGGTTAGT 849
 XX

QY 899 GTATCATGGGAGCAACATTCATACTGCTCCGAATGAGTCGGACGAA 958
 Db 850 ACAGGTTGGTGGAAAGGAAACCTTAACCTTCATCATGCTGCTCCAAATGATCAG 909
 QY 959 CAGTACACACTCTAACGAGACATTGATACTCTCCCCATCATCATGCTGCTCCAAATGATCAG 1018
 Db 910 ACTTACCAACAAATTGATGAGATATTGATACTCTCCCCATCATGCTGCTGGAGCAAGGAC 969
 QY 1019 ATTTGGCACCGTGTAGAGCAGAGAATTTCGAGGTGCTTCATAATCAGCACTACATG 1078
 Db 970 ATACTGGCACAGTGTAGAGATTCAGACATTCTGCGAATCTCCAAATACCAAGCATCTGTTC 1029
 QY 1079 ATTCTGCTCTATGTTCAATGGCCGGTACAGTTGGACTTTGGAAAGTTCTCTTCACA 1138
 Db 1030 TTCAATGTTCTGTTATTTGCCCGTGGTAGTTGGCTCTTGGAGGTGAGATAACC 1089
 QY 1139 TTCAATCTGATTGGCACGACCAAGGGATTGATAGAGAAGGGAAACAGTTGCTTCTCAC 1198
 Db 1090 TCTACAGCAGTGTCTCACCTGTCGACAGGTGTTGAGAAAGGGAACTGTTCTGTTCAC 1149
 QY 1199 TAGGCCTGGTCCATATTTCGGGGCTCGGGCTCAGTGGCTAAAGCCCTCTTGCCTGCG 1258
 Db 1150 TACTTTGGTTCGTCGGCTATCITCTCCCTGGT--TGGAAGCCATTAGTA 1206
 QY 1259 TGGATGGTAGCAAACTGAGCTTGGCCGGTTGGGGATTCTGGTTACGTTGAGT 1318
 Db 1207 TGGATGGGGTAGCTAGTCAGGGTGTGGCGATGGCTGTGGCTTGTGTTACTTAGC 1266
 QY 1319 CACAATGAAAGGGTTTACATGAAGGACTTGTGAGAGGCCMGGTTATTACCC 1378
 Db 1267 CACAATGGGATGGTTATAATTGGCTTAAAGAATTGGCTGAGTCGACATGTGTAC 1326
 QY 1379 ACCCGTAACACCAAGGGCTGGTTCAACGATTGGTCACTGGGGACTCGACACCCAG 1438
 Db 1327 ACACGGGATATCAAGGAAACATATTCAACGACTGGTCACTGGGGCTAACAGGCA 1386
 QY 1439 ATTGGCATCACCTGTTCCAACAAATGCCAGGCAACACTACCCAGATGCCACCTCAG 1498
 Db 1387 ATAGAGCATCATCTTCCCAACAAATGCCAGGCAATAATTAAACAAAATAGCACCTAGA 1446
 QY 1499 GTCGAGGTCTTTGAGGCAAGGCACGGCCTCGAGTACGATAATGTCCTGGTGTGCC 1558
 Db 1447 GTGGAGGTCTCTGTAAAGAACACGGCTCTGGTGTACAGACGTATCTATTGCTACCGGC 1536
 QY 1559 TCTGTGGCTCAAGGAAATTGCTGATGAAGGGTCAATTGGCTT 1615
 Db 1507 ACTTGCAAGGTTGAGCATTTGAGATGAAAGGAAGTGGGCTSGGGCAGGAGCAT 1563
 RESULT 5
 ABQ76782
 ID ABQ76782 standard; cDNA; 1578 BP.
 XX
 AC ABQ76782;
 DT 25-MAR-2003 (first entry)
 DE P. patens D6 desaturase cDNA SEQ ID 7.
 XX Promoter; expression cassette; structural gene; plant; transgenic;
 KW Linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
 KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 KW heart disease; seed-specific; gene; ss.
 XX physcomitrella patens.
 XX Key
 F3 Location/Qualifiers
 1. .1578
 FT /*tag= a
 FT /product= "D6 desaturase"
 XX DE10102338-A1.
 PN CTCCTGTCACAACAGTGTGGATGGCTTCCATCAACAGGTCTTGGAG 838
 XX

PD 25-JUL-2002.
 XX
 PR 19-JAN-2001; 2001DE-C1002338.
 XX
 PA (BADI ; BASF PLANT SCI GMBH.
 XX
 PI Lerchl J., Duwenig E., Bischoff F., Heinz E., Drexler H., Scheffler J.;
 XX
 WPI; 2002-675961/73.
 DR
 P-PSDB; ABG73602.
 XX
 New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids.
 XX
 Example 17; Page 64-67; 188pp; German.
 XX
 This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-) functional nucleic acid in the vector. Transgenic plants e.g. linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the invention
 XX
 Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;
 SQ Query Match 27.8%; Score 567.4; DB 6; Length 1578;
 Best Local Similarity 66.3%; Pred. No. 3.8e-130;
 Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;
 XX
 QY 359 ACTTACTCTGGCCGATGTTGCTTCACGACAGGCCGACTGCTGGATGATCGTC 418
 Db 313 ACACACCCCTATCAGAAGTAGCTGAGTCAGTCACACAAGCCAAAGGATTGTTGTA 369
 QY 419 AAAGAGAAGGGTGTATGATATTAGCCGTTTGCGACGCCACCCGGAGGAGGTAAATT 478
 Bb 370 AAAACRAGGTGTATGATGTTCCAAATTGGACGAGCAAGATGGCAGTCAGTTATT 429
 QY 479 AGCACCTACTTTGGCGGGATGGCACAGACGTTTCGCAACATCCATCCACCTGCCGCA 538
 Db 430 AGTACTTATTGGACGAGCAAGCTTACATTGGTACATGGTACGTTCTACAC 489
 QY 539 TGGAGCAACTCAATGACTACATTGGAGACCTTGTGCTGAGCCCCTGTATGTA 598
 Db 490 TGGAAAATTCTCAAGACTTTACATTGGTACGTTCTACAC 549
 QY 599 TTGCTTAAGAAGTACAGAGATATGAGAGCCGAGTTGTTAGAGAAGGGCTTTAGAGT 658
 Db 550 CTGCTGAAAGATTCCGAGAATGGAGCTCTTCCCTGAGGGAGCAACTTTCAAAGT 609
 QY 659 TCCAAGGGCTGGTCTGTTACGACAAGAGTACTGGGTATTGCTGTCAGCCAGTTGATGGGT 718
 Db 610 TCGAAATTGTTACTATGTTATGAAAGCTGTCACGAATGTTGCTGAGGAGCAT 669
 QY 719 CGGACTATCTGTTACGACAAGAGTACTGGGTATTGCTGTCAGCCAGTTGATGGGT 778
 Db 670 CGATAATGTTGGAGCAAGACTTTACGTTCTACAGTTGCTGATGATGGCT 729
 XX

QY	659	TCCAGGCCCTGGTTCTCTGCTTCAACTCTGATTAATGCGACTCTGCTCTTCGAGGCAATT	718	DT 28-MAR-2003. (first entry)
Db	928	TGAAATGTGACTAATGTTATGAAAGCTGCTCACGAATGTTGCTTGTGAGGCAATT	987	DE Plant specific expression vector expressing desaturase SEQ ID NO 25.
QY	719	GCGACTATCTGTTACGACAAGGTTACTGGCTATTGGCTTGTGAGGCAATT	778	KW Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
Db	988	GCAATAATATGTTGGAGCAAGACTATTCAAGGGTTTTGGCTTGTGATGGCTT	1047	KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
QY	779	CTCTTCTGTCACAGTGTGGATGGCTTACATCAACAGGACTTTGAG	838	KW plant; elongase; gene; ds.
Db	1048	CTGTGTTCCAACAGTGGCTTAAATGAAAGTGGCTATCCCATGATTCTCCACAAATCG3GTGAG	1107	OS Phaeodactylum tricornutum.
QY	839	AACCGTACCCGGAAACTCCCTCTTGGCTATTGGTGGCAAATTGGTGCTTGTGCTTGTAGT	898	OS Physcomitrella patens.
Db	1108	ACACGCTGGCTTAATGAAAGTGTGGGTATGTGATGGCAAACTG3GTGAG	1167	OS Synthetic.
QY	899	GATATCAGTGGAGGACGACAACTCATCATGCTCCGAATGAGS1GCGACGA	958	OS Chimeric.
Db	1168	ACAGGGTGGTGGAAAGGAGCATACCTTCATCATGCTGCTCCAAATGAATGGCGATCAG	1227	XX
QY	959	CAGTACACACCTCTGACCAAGACATTGATACTCTCCCAATCATGGCAACTCATG	1018	Key Location/Qualifiers
Db	1228	ACTTACCAACATTGATGAAGATAATTGATGATGACTCTCCCCTCATGGCTGGGCAAGGAC	1287	CDS 11543 . -12415
QY	1019	ATTTGGCCACCGTTGAGGAAAGAACATTGAGATAAGACATTGAGAATTCATGGCTTCAATCATGCACTCATG	1078	/*tag= a
Db	1288	ATACTGGCCACAGTTGAGAATAAGACATTGAGATAAGACATTGCGATCTCCAAATACCGAACATCTGGC	1347	/product= "elongase"
QY	1379	ATTCCTGCCTTATGGTTCATGGCCGGTACAGTGGACTTTGGAAAGTTGCTCTTCACA	1138	/note= "ABB98278"
Db	1348	TTCAATGGGTCTGTATTGGTGGAGGATATTGATGACTCTCCCCTCATGGCTGGGATAAAC	1407	CDS 13313 . -14890
QY	1139	TTCATGTTGAGGAAAGGATTGATGAGAAGGGCAACGACTTTTCAC	1198	/*tag= b
Db	1408	TCTACAGGAGTGTGCTCACCTGTGACAGGTTGTTGAGGAAAGGAAACTGTTCTTCAC	1467	/product= "desaturase"
QY	1199	TACGCCTGGTTCACTGTGGCTTCCATATTGGCGGGTGTGCTAAGCCTCTTGC	1258	/note= "ABB98277"
Db	1468	TACTTTTGGTTGGTGGTGGAGGCTCTCCCTGGTGTGGCTTGGAGGATATAAC	1524	XX
QY	1259	TGGATGGTAGCAACTGAGCTTGTGGCTGGTTGGGATTCTGGTGTGGTTACGTTGAGT	1318	XX
Db	1525	TGGATGGGGGTGACTGAGCTCATGTCCGGGATGGCTTGTGGCTTGTGTTGACTT	1584	XX
QY	1319	CACAAATGGAAAGGGTTACATGAATGAACTGAAAGGACTTCGTGAGGAGCCAGGTATTAC	1378	CC The invention relates to preparing (M1) fatty acid esters (I) with an
Db	1585	CACAAATGGATGGGGTTATAATTGCTCTAAAGAAATTGAGTGGCATGATCGTATCC	1644	CC increased content of polyunsaturated fatty acids (II) with at least two
QY	1379	ACCCGTAACACCCAAGGGCTGGTTCAACGATTTGGTCAACTGGGGACTCGAACACCCAG	1438	CC double bonds by introducing into a (I)-producing organism a specific
Db	1645	ACACGGGATATCAGGAAACATATTCAACGACTGGTGGCCTTAACAGGCAA	1704	CC nucleic acid (A). (M1) is useful for preparing ester containing
QY	1439	ATTGAGGATCACCTGTTCCAAACAAATGCCOAGGCACACTACCTGGGACTCGACCTCAG	1498	CC polyunsaturated fatty acids. Oils, lipids and (II) or their fractions,
Db	1705	ATAGAGGATCACATCTTCCAAACAAATGCCOAGGCATATAACAAATAGCACCTAGA	1764	CC produced by (M1) are used in animal and human nutrition, cosmetics and
QY	1499	GTGGAGGGTCTGTAAGAAACAGGTTCAACGATTTGGTCAACTGGTGGCTTGTGCT	1558	CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
Db	1765	GTGGAGGGTCTGTAAGAAACAGGTTCAACGATTTGGTGGCTTGTGCT	1824	CC the blood and to protect against heart disease. Cells that express (A)
QY	1559	TCTGTGCGGGTTGTGAAAGGAATTGCTGATGAAGGCCAATTGCGCTT	1615	CC are also used to identify (ant)agonists of desaturases, e.g. for
Db	1825	ACTGCAAGGTTGAAAGCATGAAAGGAATTGCTGATGAAGGCCAAGGAGCAT	1881	CC modulating the yield and rate of production of particular fine chemicals
QY				CC in microorganisms (claimed). Also (A) and derived proteins can be used as
Db				CC markers of specific genomic regions and in evolutionary/protein
QY				CC structural studies. (M1) is suitable for large scale production (no known
Db				CC biotechnology method can produce (II) on a useful scale). The present
QY				CC sequence is that of the pUC19 based plant specific expression vector
Db				CC (ABV74272) expressing the Physcomitrella patens elongase (ABB98278) and
QY				CC the Phaeodactylum tricornutum desaturase (ABB98277) of the invention.
Db				CC (Updated on 07-AUG-2003 to correct OS field.)
QY				XX Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;
Db				SQ Query Match 27.8%; Score 567.4; DB 6; Length 15430;
QY				Best Local Similarity 66.3%; Pred. No. 8.9e-130; Mismatches 0; Indels 3; Gaps 1;
Db				Matches 833; Conservative 0; ACV74274 standard; DNA; 15430 BP.
QY				XX 359 ACTTACTCTGGCCGATGTTGCTCTCACGACAGGCCCTGGACTGCTGGATCGTC 418
Db				DB 13622 ACACACCCCTATCAGAAGTAGGAGCTACACAGCCAAAGCAACAGCTACAGTGTGTTGTA 13681

Qy	419	AAAGAGAAGGTGTTGATATTAGCCGTTTGGGAGGACCCCTGGGAGGACGGTTAATT	478	Db	14759	GTGGAGGAGGTTCTTAAGAACACGGTCTGGTACGAAGCTTACCGGCCTACGGGC	14818
Db	13682	AAAACAACTGGTATGTTCAATTGGGAGGATCAGTATTGGGACAGCATCCGGAGGATCAATT	13741	Qy	1559	TCTGTGGGGTTGTTGAAAGGGCTCAAGGAAATTGCTGATGAAAGGGCTATTGGGCT	1615
Qy	479	AGCACCTACTTTGGGGATGCCAACATCCATCCACCTGGCGCA	538	Db	14819	ACTTGCAAGGTTTGAAGCATTGCGGAGGGCTGCGGAGGAGCAT 14875	
Db	13742	AGTACTTATTGGACAGAACGGCACAGATGTTCTAGTTCATGAGCTTCATA	13801				
Qy	539	TGGAAGCAACTCAATGACTACAGAGATAATGAGGCCAGTTCTAGGAAAGGGCTTCAAGAGT	598				
Db	13802	TGGAAGAAATTCTTCAGACTTTACATGGTAGACGTGAGAGCTTCAAAAGT	13861				
Qy	599	TTCGTTAAAGACTACAGAGATAATGAGGCCAGTTCTAGGAAAGGGCTTCAAGAGT	658				
Db	13862	CTGTGAAAGATTCCGAGLARTGAGGCTTCTCTGAGCTTCAAAAGT	13921				
Qy	659	TCCAAGSCTGGTTCTCGCTCAGACTCTGATTAAATGCCAGCTCTTGCAGGATT	718				
Db	13922	TGGAATTGTAATGTTATGAAAGCTGCTAACGAATGTTGCTATTTGCTGAGGATT	13981				
Qy	719	GCGACTATCTGTTACSGAACAGGTTACTGGCTTATTGGCTTCASSCAGTTGATGGGT	778				
Db	13982	GCAATAATATGTTGGAGCAAGRACTATTGCGTTCAAGCTTCAAGTTGATGGCT	14041				
Qy	779	CTCTCGTCCAACAGTGGATGGCTTCCCTCATGATTCCTCATCAAACAGGTCTTGAG	838				
Db	14042	CTGTTTCCAACAGTGGATGGCTATCCATGATTCTCATACATCAAGGTGTTGAG	14101				
Qy	839	AACCGTACCGGAACCTCTTGGCTTATTGTTCCGCTTGCSTGCTTGGCTTAGT	898				
Db	14102	ACAGCTGGCTTAATGAAAGTGTGGGTATGTGATCCCCTTCTGGGTTAGT	14161				
Qy	899	GTATCATGGGGAGGACAAACATTCAATCATGCTCGAATGAGTGGCAGCAA	958				
Db	14162	ACAGGGTGGTGAAGGAGAACATTAACCTTCATCATGCTCAAATGAATGGCATG	14221				
Qy	959	CAGTACACACTCTAGAGAACATTGATACTCTCCCCATCATTTGCCCTGGAGGAA	1018				
Db	14222	ACTTACCAACCAATTGATGAAAGTATTGATACTCTCCCCCTCATTTGCCCTGGAGGAC	14281				
Qy	1019	ATTITGGCCACCCGGTGGAGGAAATTGGCTCAGATATCAGCACTACATG	1078				
Db	14282	ATACTGGCCACAGGTGGATTAAGACATTCTGGAAATACGATCTGGTTC	14341				
Qy	1079	ATTCTGCCTCTATTGTTCATGGCCGGTACAGTGGACTTTGGAGTTGCTCTTACA	1138				
Db	14342	TTCATGGGTCTGTTATTTCGCCCGTGGTAGTTGCTCTTGGAGCTGGAGATATAACC	14401				
Qy	1139	TTCAATCCTGATTGGCAGGACCAAGGGATTGATAGAGAACAGTTGCTTTCAC	1198				
Db	14402	TCTACAGGAGTGGCTCTACCTGTGGACAGGTTGGT3GAGAACTGTTCTGTTTCAC	14461				
Qy	1199	TACGCCCTGGTCAAGTGGCTGCCATTATTTGCCGGTGTGCTTAAGCCTCTTGC	1258				
Db	14462	TACTTTGGTCTGGTCTCCTGGCTATCTTCTCCCTGGT---TGGAAAGCCATTAGTA	14518				
Qy	1259	TGGATGGTAGCAACTGAGCTGGCTGGGGATCTGGTTACGTTGAGT	1318				
Db	14519	TGGATGGGGTGTGACTGGCTCATGTCGGCATGCTGCTGGCTTGTGTTACTAGC	14578				
Qy	1319	CACATGGAGGTTTACAATGAAATGAGGACTTGGCTGAGGCTTATTCAC	1378				
Db	14579	CACATGGGATGGAGGTTTAAATTGCTAAAGAATTCGTTGAGTGGCTGACAGATCGTATCC	14638				
Qy	1379	ACCGTAACACCAAGGAGGCTGGTCAACGATTGGTTCACTGGGGACTCGACACCCAG	1438				
Db	14639	ACACGGGATATCAAAGGAACATATTCAACGACTGGTCACTGGTGGCCCTTAACGGCAA	14698				
Qy	1439	ATTGAGCATCACCTGTTCCAAACATGCCAGGACAACTACCCAAAGATCGCACCTCAG	1498				
Db	14699	ATAGAGCATCATCTTCCAAACATGGCCAGGCTAAATAGCCACCTAGA	14756				
Qy	1499	GTGCAAGGGCTCTTGGCAAGGAAGGCCGGCTGGAGTACGATAATTGCTCCCTGGTGGCC	1558				

SQ	Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 375-B T; 0 U; 0 Other;	QY	1379 ACCCGTAACACCAAGGAGGGCTGGTTCAACGATTG3TTCACTGGGGACTCGACACCCAG 1438
Query Match	27.8%; Score 567.4; DB 6; Length 15430;	DB	14639 ACACGGGATATCPLAAGAAACATATTCAAACGACTGGTCACTGGTCCCTTAACAGGCAA 14698
Best Local Similarity	66.3%; Pred. No. 8.9e-130;	QY	1439 ATGGAGCATCACCTGTTCACATGCCAACAGTACACTACCCAAAGATCGCACCTCAG 1498
Matches	833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;	DB	14699 ATAGAGCATCATCTTTCACATGCCAACATGGCCAGTAAATAGCACCTAGA 14758
Qy	359 ACTTACTCTTGCCCGATTTGCTCTCACGAGGCGCTGGAGACTGCTGGATGATCGTC 418	QY	1499 GTCGAGGCTCTTTGCAAGAACGGCCTCGAGTAGCTAAATGTCCTCCGTGTTGGTGC 1558
Db	13622 ACACACCCCTATCAAGTAGCTACAGTACRPLACAAGCAGGATTTGGTGGTTGTA 13681	DB	14759 GTGGAGGTGTTCTGTAAAGAACACGGTCTGGTACGAAGACGTATATTGCTACCGGC 14818
Qy	419 AAAGAGAAGGGTGTATGATATTAGCGTTTGCGAACCCCTGGAGGAGCGGTAAAT 478	QY	1559 TCTGTGCGGTTGTGAAGGGCTCAAGGPLATTGCTGATGAAGCGTCAATTGGCTT 1615
Db	13682 AAAAACAGGGTGTATGATGTTGGGAGGATTTGGGAGGATCCGGAGGTCAAGTAT 13741	DB	14819 ACTTGCAAGGTTTGTAAAGCATTGAGGAAGTCGGGAGGCTGGAGGACAT 14875
Qy	479 AGCACCTACTTGGGGGATGGCACAGACGTTTCGAACATCCACATGCCGCA 538		
Db	13742 AGTACTTATTGGGAGGAGACGSGCACAGATGTTTCTCTAGTTTCATGCAGCTTCTACA 13801		
Qy	539 TGGAAAGGCAACTCAATGACTACATTGGAGACCTTGCTAGGGAGAGGCCCTGTGATGAA 598		RESULT 10
Db	13802 TGGAAAATTCTTCAAAGACTTTAACATTGGTGAAGTGGAGCCGACTCCAGAG 13861	ABV74275	
Qy	599 TTGCTTAAGAAGTACAGAGATAATGAGAGCCGAGTTGGTTAGAGAACGGCTTTCAAGACT 658	ID	ABV74275 standard; DNA; 17752 BP.
Db	13862 CTGCTGAAAGAATTTCCGAGAAATTGAGAGCTCTTTCTAGGGAGCAACTTTCAAAGT 13921	XX	
Qy	659 TCCAAGGGCTGGTTCTGCTTCAAGACTCTGATTAAATGCACTCTTGGTGGAGGCACT 718	AC	ABV74275;
Db	13922 TCGAAATTGTTACTATGTTATGAAGGTGCTCACGAATGTTGCTATTGCTGGAGCACT 13981	XX	07-AUG-2003 (revised)
Qy	719 GCGACTATCTGTTACAGACAAGGTTTACCTGGGCTATTGGCTGTGTCAGCTTGGGGT 778	DE	DT 07-AUG-2003 (first entry)
Db	13982 GCAATAATATGTTGGAGCAAGGCTATTTCAGGGTTTGGCTTCAAGCTTGTGATGGCT 14041	XX	Plant specific expression vector expressing desaturase SEQ ID NO 28.
Qy	779 CTCCTCGTCCAACAGGTGGTGGCTGGCCATGATTTCCTTCACAGGTCTTTGAG 838	KW	Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
Db	14042 CTGTTTCCAACAGTGGGATGGCTATCCATGATTTCCTCCAAATCAGGTGTTGAG 14101	RW	animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic; plant; elongase; gene; ds.
Qy	839 AACCGTACCGGAAACTCCCTCTTGGCTATTGGCTGATGAGCTGGTTAGT 898	XX	Phaeodactylum tricornutum.
Db	14102 ACACGCTGGCTTAATGAAGTTGGTATGGTACGGTCACTGGATCG 14161	DE	Physcomitrella patens.
Qy	899 GTATCATGGGAGGACAACATCATCATCGTCCTGAAATGAGTGGGACGAA 958	CS	Synthetic.
Db	14162 ACAGGGTGGGAGGAAAGGAGGAAACCTTCATCATCGTCCTGCTCAAATGAAATGGATCAG 14221	OS	Chimeric.
Qy	959 CAGTACACACCTCTGAGCAAGACATTGATACTCTCCCACATCATGCCCTGGAAAGGAA 1018	XX	
Db	14222 ACTTACCAACCAATTGATAAGATAATTGATACTCTCCCCTCATGCCCTGGGAGGAC 14281	DE	
Qy	1019 ATTTGGCCACCGTTGAGGAGAGATTGGGASTGGCTCAATATCAGGACTACATG 1078	CS	
Db	14282 ATACTGGCCACAGTGGAAATAAGACATTCTGGGAACTTCCCAATACAGGATCTGTC 14341	OS	
Qy	1079 ATTCTGCCTCTATTTCATGGCCGGTACAGTTGGACTTTGGAAAGTTGGCTCTTCACA 1138	XX	
Db	14342 TCTACAGCAGTGGCTCTCACCTGTGCAAGCTGGTGGAGGAACTGTTGTTCAAC 14401	PN	DE101023337-A1.
Qy	1139 TICAATCTGTGTTGAGCACGACCAAGGGAACTGATAAGAGAACAGTTGGCTCTTCACA 1198	XX	25-JUL-2002.
Db	14402 TCTACAGCAGTGGCTCTCACCTGTGCAAGCTGGTGGAGGAACTGTTGTTCAAC 14461	PD	
Qy	1199 TACGCCCTGGTTCAAGTGGGCTCCATATTGGCTGGCTAAGGCTCTTGC 1258	XX	PR 19-JAN-2001; 2001DE-01002337.
Db	14462 TACTTGTGGTGGCTGGGACAGGGTGCTATCTCCCTGGT--TGAAGCCATTAGA 14518	XX	PA (BIDI) BASF PLANT SCI GMBH.
Qy	1259 TGGATGGTAGCAACTGAGCTGGTGGGATTTGGTTACGTTGGT 1318	XX	XX
Db	14519 TGGATGGGTGACTGAGCTGAGCTGGCTGGCTTGTATTTGACTTGGC 14578	PT	Preparing ester containing polyunsaturated fatty acids, useful e.g. in animal or human nutrition, by transforming organism with desaturase gene from Phaeodactylum tricornutum.
Qy	1319 CACAATGAAAGGAGGTTAACATGAATGAAAGGACTCTGTGAGGCCAGGGTATTAC 1378	PT	Example 11; Page 154-170; 182PP; German.
Db	14579 CACAATGGGATGGAGGTTATAATTGCTAAAGAATTCTGTTGAGTCACAGATCGTATIC 14638	PS	XX

The invention relates to preparing (M1) fatty acid esters (I) with an increased content of polyunsaturated fatty acids (II) with at least two double bonds by introducing into a (II)-producing organism a specific nucleic acid (A). (M1) is useful for preparing ester containing polyunsaturated fatty acids. Oils, lipids and (II) or their fractions, produced by (M1) are used in animal and human nutrition, cosmetics and pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. Cells that express (A) are also used to identify (anti)agonists of desaturases, e.g. for modulating the yield and rate of production of particular fine chemicals in microorganisms (claimed). Also (A) and derived proteins can be used as markers of specific genomic regions and in evolutionary/protein structural studies. (M1) is suitable for large scale production (no known bioengineering method can produce (II) on a useful scale). The present sequence is that of the pUC19 based plant specific expression vector (ABV74273) expressing the Physcomitrella patens elongase (ABB98278) and the Phaeodactylum tricornutum desaturase (ABB98277 and ABB98274) of the invention. (Updated on 07-AUG-2003 to correct OS field.)

XX Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;
 Query Match 27. 8%; Score 567.4; DB 6; Length 17752;
 Best Local Similarity 66.3%; Pred. No. 9.3e-130;
 Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;

QY	359 ACTTACTCTGCCGATGTTGCTTCAGACAGCCCTGGAGACTGCCGGATCGTC 418	Db 13622 ACACACCCCTATCAGAAGTACACAAGCCAAAGCAACAAATGCGATTGTTGTA 13681
QY	419 AAAGAGAAAGGTGTATGATATTAGCCGTTTGCGGACGACCACCCGGGGACGTTAATT 478	Db 13682 AAAAACAAAGGTGTATGATGTTCCAATTTCGGGAGGAGCATCCGGAGATCAGTTATT 13741
QY	479 AGCACCTACTTTGGGGATGGCACAGCTTTGCCAACATCCCATGCCGCA 538	Db 13742 AGTACTTATTGGACGAGCAGGACAGATGTTCTCATGCAGCTTCA 13801
QY	539 TGGAAAGGAACTCATGGAGACCTTGTCTAGGGAGGCCCTTGATGAA 598	Db 13802 TGGAAAATTCCTCAAGACTTTACATGGGTGACGTGGAGGGTGGAGCCAGAG 13861
QY	599 TTGCTTAAGACTACAGAGATGAGAGCGAGTTGTTAGAGAAGGGCTTCAAGAGT 658	Db 13862 CTGCTGAAGATTTCCGAGAATGGAGCTCTTCTGGAGCAACTTCAAAGT 13921
QY	659 TCCAGGCCCTGGTCTGCTTCAAGACTCTGATAATGCAGCTCTGGAGCATT 718	Db 13922 TCGAAATTGTACTATGTTATGAAAGTGTCTACGAATGTTGCTATTTCTGGAGCATT 13981
QY	719 GCGACTATCTGGTAGCAAGAGTTACTGGCTATATGCTGTCAGCCAGTTGATGGGT 778	Db 13982 GCAATTAATGTGGAGCAAGACTATTTCAGGGTTGGCTTCAAGCTGTATGATGGCT 14041
QY	779 CTCTTGTCCAACAGTGTGGATGGCTTCAAGGTTCTTGCTTCA 838	Db 14042 CTGTGTTCACAGTGTGGATGGCTATCCCATGATTTCGGTTGGCTTCAAGCTGTATGATGGCT 14101
QY	839 AACCGTACCGGGAACCTCCTGGAGCAACATCAACTGCTCCGAATGACTSGACGA 958	Db 14102 ACACGGTGGCTTAATGAAGTTGTGGGTATGTGATGGCAACGGCTTGTGTTAGT 14161
QY	959 CAGTACACACCTCTAGACGAAGCATTGATACTCTCCCCATCATGGCTGGCAATTGGCTTCA 1018	Db 14222 ACTTACAAACATTGTAAGATATTGATACTCTCCCCTCATGGCAAGGAC 14281
QY	1019 ATTTGGCCACCGTTGAGCAAGAATTGGCAGTGTGCTCAATATCAGCACTACATG 1078	Db 14282 ATACTGGCACAGTTGAGAATAAGACATTGCGAATCTGTC 14341

QY 1079 ATTCTGCCTCTATTGTTCATGGCCGGTACAGTTGGACTTGGAAAGTTGCTTTCACA 1138
 Db 14342 TTCATGGGTCTGTATTTTCGCCCGTGTGTTAGTGGCTTGGAGATAATGCC 14401
 QY 1139 TTCATCCTGATTGAGCAGCAAGGGATTGATAGAGAAGGGAAACAGTTGCTTTTCAC 1198
 Db 14402 TCTACASCGTGTCTCACCTGTGGACAGGTTGTGGAGAAGGAACACTGTTGTTTCAC 14461
 QY 1199 TAGGCCTCAGTTGCTGGCTCAAGGCTTGTGCG 1258
 Db 14462 TACTTTGGTTGTCGGGACAGGGTGTATCTCTCTCCCTGGT--TGGAGCCATTAGTA 14518
 QY 1259 TGGATGGTAGCAACTGAGCTTGGGGATTGGTGGTAACTGTTGAGTTGAGT 1318
 Db 14519 TGGATGGGGTCACTGAGCTCATGTCGSSCATGTCGTCGGCTTGTATTGTACTTAGC 14578
 QY 1319 CACATGGAAAGGGTTTACAATGAATGCAAGGACTTGTGAGAGGCCAGGTATTAC 1378
 Db 14579 CACATGGATGGGGTTTAAATTCGTCATAAGAATTGTCAGATCGTATCC 14638
 QY 1379 ACCCGTAACACCAAGGCTGGTTCAACGATTGGTTCAGTGGGGACTCGACACCCAG 1438
 Db 14639 ACACGGGATATCAAGGAACATATTCAACGACTGTTTACACTGGCTTAACAGGCAA 14698
 QY 1439 ATTGAGCATCACCTGTTCCAAACATGGCCAGGACAACATACCCCAAGATGCACTCTAG 1498
 Db 14699 ATAGAGCATCACCTTCCCAACAAATGCCAGGATATTAAACAAATAGCACTTGA 14758
 QY 1499 GTCGAGGGCTCTTGGCAAGAACGGCCTCGAGTACGATAATGTCCTCGTGTGGTGCC 1558
 Db 14759 GTGGAGGTCTCTGTAAGAAACACGGTCTGGTGTACGAAAGCTATCTATTGCTACCGGC 14818
 QY 1559 TCTGTGCGGGTTGAGGGAAATTGCTGATGAAGGGTCAATTGGCTT 1615
 Db 14819 ACTTGCAAAGGTTTGTAAGGATTCAGGATTAAGGAGGCT 14875
 RESULT 11
 ABQ76797 ID ABQ76797 standard: DNA; 17752 BP.
 XX AC ABQ76797;
 XX DT 25-MAR-2003 (first entry)
 XX DE DE
 XX KW Promoter; expression cassette; structural gene; plant; transgenic;
 KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic;
 KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 KW heart disease; seed-specific; ds.
 XX OS Physcomitrella patens.
 OS Phaeodactylum tricornutum.
 OS Synthetic.
 XX Key CDS
 11543. .12415
 /*tag= a
 /product= "delta6 elongase"
 /note= "from Physcomitrella patens"
 13313. .14890
 /*tag= b
 /product= "delta6 desaturase"
 /note= "from Physcomitrella patens"
 15791. .17200
 /*tag= c
 /product= "delta12 desaturase"
 /note= "from Phaeodactylum tricornutum"
 XX PD DE10102338-A1.
 XX 25-JUL-2002.

XX	19-JAN-2001; 2001DE-01002338.	898
XX	(BADI) BASE PLANT SCI GMBH.	958
XX	Ierchl J, Duwenig E, Bischoff F, Heinz B, Drexler H, Scheffler J;	14161
XX	WPI ; 2002-675961/73 .	14102
DR	P-PSDB; ABG73608, ABG73610,	ACAGGCTGGCTTAATGAAGTGTGGTCAAGCGACGAA
PT	PT	GTATCATGGAGGAAAGGATAACCTCATCATGCTCCGACGAA
PT	PT	1018
XX	New expression cassette for plant genes, useful for preparing transgenic plants that have increased production of polyunsaturated fatty acids.	959
PS	Example 13; Page 158-174; 188PP; German.	CAGTACACACCTCTAGAACAGACATTGATACTCCTCCATCATTGCTGGAGCAAGGAA
XX	This invention describes novel expression cassette (EC) containing at least one each of plant promoter (P) and structural gene (SG) expressed in plants, flanked by specific restriction enzyme (RE) recognition sites. The EC has the structure (L1-P-SG-L2) where L1 = is a polylinker (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker sequences reproduced (ABQ76799-ABQ76801); or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this EC, an organism containing the EC or the vector and a transgenic plant containing a (non-) functional nucleic acid in the vector. Transgenic plants e.g. linseed can be prepared with improved content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the invention	1019
XX	Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;	TTGGAGGAAAGGGTTTACAAATGAATGAAATGGCTTCCATGGGACAGCCACCTGGGATGTCGTC
SQ	Query Match 27.8%; Score 567.4; DB 6; Length 17752; Best Local Similarity 66.3%; Pred. No. 9.3e-130; Matches 833; Conservative 0; Mismatches 421; Indels 3; Gaps 1;	13622 ACACACCCCTATCAGAAGTAGCAGTACACAAAGCCAAGGGATTGCTGGATTGTGTA
Db	359 ACTTACTCTGGCCGATGTTGCTCTCAAGACAGGCCCTGGAGACTGCTGATGTCGTC 418	13682 AAAACAAGGTGTATGATGTTCCATTITGGGACAGGACATCCGGGAGGATCAGTTATT
QY	419 AAAGAGAAGGTGTATGATATTAGCCGTTTGGGACACCCTGGGGACGGTAAATT 478	479 AGCACCTACTTGGGGGGATGGCACAGCTTCCAAACATCCATCCACCTGCCGCA
Db	Db 13682 AAAACAAGGTGTATGATGTTCCATTITGGGACAGGACATCCGGGAGGATCAGTTATT 13741	Db 13742 AGTACTTATTGGACAGGACGGCACAGATTCTCTAGTTTCATGCCAGCTTCTACA 13801
QY	539 TGGCTTAAGACTCAATGACTACTCATGGAGACCTTGCTAGGGAGGCCCTTGATGAA 598	RESULT 12
Db	Db 13802 TGGAAAATTCTCAAGACTTTACATTGGTACGTGGAGGGCAACTTCAAAAGT	AAF25731
QY	599 TTGGCTTAAGACTACAGAGATTCAGAGCCGAGTTGGTAGAGAGGGCTTCAAGAGT 658	ID AAF25731 standard; DNA; 520 BP.
Db	Db 13862 CTGGCTGAAGATTCCGAGAATTCAGAGCTTCTGGCTTCCCTGAGGGCAACTTCAAAAGT	XX AAF25731;
QY	659 TCCAAGGCCCTGGTCTGGCTCAGACTCTGATAATGCAAGCTCTGGCTGGAGCATT 718	XX DT 06-APR-2001 (first entry)
Db	Db 13922 TCGAAATTGTAATGTTATGAAGGCTGCTCACGAATGTTGCTTGGCTTCAAAAGT	XX C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 5.
QY	719 CGGACTATCTGTACGACAAGAGTTACTGGGCTTATGCTGTCAGGCCAGTTGATGGGT 778	XX XX Delta6-acetylase; delta6-desaturase; unsaturated fatty acid; transgenic plant; plant oil; triglyceride; nutrition; animal feed; cosmetic; ds.
Db	Db 13982 GCAATAATATGTTGGAGCAAGACTATTTCAGGCCGTTTGGCTTCAAGATGGCT 14041	XX OS Ceratodon purpureus .
QY	779 CCTCTCGTCCACAGTGTGGATGGCTTCTATCAACAGGTCTTGAG 838	XX PN WC200075341-A1.
DDB	DDB 14042 CTGTTCTACACAGTGGGATGGCTATCCATGATTTCAGGCCAGTTGAG 14101	XX PD 14-DEC-2000.

XX	37-JUN-2330;	2000WO-EPO05274.	Db	421 ATCGAAGGAACTTCGTGAGAGGCCAGGTTATTACACCCTAACCAAGCAGGCTGGTT	480		
PF			QY	1405 CAACGATTGGTTCACTGGGACTCGACACCCAGATTGAG	144		
XX	07-JUN-1939;	99DE-01025718.	Db	481 CAACGATTGGTCACTGGGGACTCGACACCCAGATTGAG	520		
PR	22-DEC-1999;	99DE-010262409.					
XX							
PA	(BADI) BASF AG.						
XX							
PI	Heinz E,	Stymne S,	Lee M,	Girke T,	Sperling P,	Zaehringer U;	RESULT 13
XX	WPI;	2001-112153;12.	Db	AAAF25732 standard; DNA; 514 BP.			
DR	P-PSDB;	AAB46437.	QY	1405 CAACGATTGGTTCACTGGGACTCGACACCCAGATTGAG	144		
XX			Db	481 CAACGATTGGTCACTGGGGACTCGACACCCAGATTGAG	520		
PT							
PT	Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.						
XX							
PS	Example 6; Page 51; 69pp; German.						
XX	This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (II), linked to one or more regulatory sequences; (c) a vector containing (II) and EC; (d) organisms containing (II), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method 'g'. (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A), or TG containing them, are useful in human homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids.						
XX	Sequence 520 BP; 124 A; 116 C; 136 G; 144 T; 0 U; 0 Other;						
SQ	Query Match 25.4%; Score 518.4; DB 4; Length 520; Best Local Similarity 99.8%; Pred. No. 3.5e-118; Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
XX							
QY	925 CATTCACTGCTCCGAATGAGTGGGACGAACTACAGTACACCCCTCTAGACGAGAGCAT	984	CC	This invention describes a novel isolated nucleic acid (I), encoding			
Db	1 CATTCACTGCTCCGAATGAGTGGGACGAACTACACCCCTCTAGACGAGAGCAT	60	CC	polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase			
QY	985 TGATACTCTCCCCATCATTGCTGGACCAAGGAAATTGGCCACCGTTGAGAGCCAGGAG	1044	CC	activity. The invention also describes (a) amino acid sequences encoded			
Db	61 TGATACTCTCCCCATCATTGCTGGACCAAGGAAATTGGCCACCGTTGAGAGCCAGGAG	120	CC	by (I); (b) an expression cassette (EC) containing (II) linked to one or			
QY	1045 AATTTTGCAGTGGACTTCAATATCAGCACTACATGATTCATGTTCAATGCCCG	1104	CC	more regulatory sequences; (c) a vector containing (II) and EC; (d)			
Db	121 AATTTTGCAGTGGACTTCAATATCAGCACTACATGATTCATGTTCAATGCCCG	180	CC	organisms containing (II), EC or the vectors of (c); (e) preparation of			
QY	1105 GTACAGTTGGACTTTCGTTCACTTAATCTGATTGAGCAAGCAGCAAA	1164	CC	unsaturated fatty acids (A) or triglycerides (TG) with increased content			
Db	181 GTACAGTTGGACTTTCGTTGGACTTTCGTTCACTTAATCTGATTGAGCAAGCAGCAAA	240	CC	of (A) by introducing (II) or EC into an oil-producing organism; (f)			
QY	1165 GGATTGATAGAGAAGGGAAACAGTTGGCTTTCACTACAGCCTGGTCACTTACAGT	1224	CC	proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)			
Db	241 GGATTGATAGAGAAGGGAAACAGTTGGCTTTCACTACAGCCTGGTCACTTACAGT	300	CC	production of (A) or TG by using (Ia); and (h) (A) and TG produced by			
QY	1225 CCATATTTGCCGGTTCGCTTAAGCCTCTGGCTGATGGTAGCAACTGAGCTTGTGCG	1284	CC	method (g). (I) are used to produce transgenic plants (or other			
Db	301 CCATATTTGCCGGTTCGCTTAAGCCTCTGGCTGATGGTAGCAACTGAGCTTGTGCG	360	CC	organisms) that produce oils or triglycerides (TG) with increased content			
QY	1285 CGGTTTGTGGGATTCTGTTACGTTGAGTCACAATGGAAAGGAGSTTACAATGA	1344	CC	of unsaturated fatty acids (A) and to isolate related sequences by			
Db	361 CGGTTTGTGGGATTCTGTTACGTTGAGTCACAATGGAAAGGAGSTTACAATGA	420	CC	homology screening. (A), or TG containing them, are useful in human			
QY	1345 ATGAAAGGAACTTCGTGAGAGCCAGGTTAACCAAGCTAACCGTAA	1404	CC	nutrition (e.g. infant foods), animal feeds, pharmaceuticals and			
Db			CC	cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can			
			CC	be used to suppress expression of (II), resulting in oils with increased			
			CC	content of saturated fatty acids			
SQ	Sequence 514 BP; 115 A; 113 C; 137 G; 149 T; 0 U; 0 Other;		XX	XX			
			Query Match 12.5%; Score 254.6; DB 4; Length 514;				
			Best Local Similarity 69.6%; Pred. No. 7.4e-53;				
			Matches 360; Conservative 0; Mismatches 154; Indels -3; Gaps 1;				
QY	925 CATTCACTGCTCCGAATGAGTGGGACGAACTACACCCCTCTAGACGAGAGCAT	984					
Db	1 CCTGCATCATGCTCCGAATGAGTGGGACGAACTACACCCCTCTAGACGAGAGCAT	60					

QY 985 TGATACTCCCATCATGGCTGGCAAGGAAATTGGCCACCGTGTGAGAGCAAGAG 1044
 DB 61 TGATACTCCCATATTGCTTGGTAAGATCTTGGCCATCTGTGAGAGCAAGAC 120

QY 1045 AATTTGGAGTGTCAATATCAGCACTACATGATTGCCTTATGGTCATGGCCCG 1104
 DB 121 CATGTTGGAGTCTCACTTACAGCACCTTGGCACTTGGTTGACGTTGCCGG 180

QY 1105 STACAGTTGGACTTTGGAACTTGCTTCACTTCAATCCTGATTGAGCACGACCAA 1164
 DB 181 GGCAGAGTGGCTATTGGAGCCCTTCACTCTAGGCCCGAGTGTGACCCCTGGCGA 240

QY 1165 CCCATTGATAAGAGMCCCACAGTTGCTTCACTACGCCCTGGTTCAAGTGGGT 1224
 DB 241 AAAGCTTGGAGAGGGAAAGGATGGCTTCACTTGGCACTACATTGGTTAATAGTGTGCGRT 300

QY 1225 CCATATTGGCGGGTGTGGCTAAGCCTCTTGGCAACTGAGCTTGTGGC 1284
 DB 301 TATATCTGGTCCCCG--ATGGAAACCAGTGTGTATGGATGGTGGTCAGGAGCTCATGTC 357

QY 1285 CGGTTTGTGTTGGATTGTTGTTACGTTGACTGCAATGGAAAGGAGGTACAATGA 1344
 DB 358 TGGTTTCCGTGGATAACGTATTGTACTCGTCAAAATGGAAATGGAGGTACAATAC 417

QY 1345 ATCGAAGGACTTCTGTAGAGGCCAGGTATTACCAACCGTAACACCAAGCGAGGGTGGT 1404
 DB 418 GTCAAAGGAGACTTCTGTGAATGCCAGATTSCATCGACTGCGACATCAAAAGCAGGGTGT 477

QY 1405 CAACGATTGGTTCACTGGGGACTCGACCCCCAGATT 1441
 DB 478 TATGATTGGTTCACCGGAGGTCTCARCGACAGATT 514

RESULT 14
 ID AAV63624 standard; cDNA; 1617 BP.
 XX AAV63624;
 AC DT 15-FEB-1999 (First entry)
 DE XX encoding a delta-6 desaturase enzyme.

XX Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

XX Mortierella alpina.

CS Key
 FT Location/Qualifiers
 FT 71. -1444
 FT /*tag= a
 FT /product= "delta-6 desaturase"
 XX WO9846763-A1.
 XX PR 11-APR-1997; 97US-0C834655.
 XX PF 10-APR-1998; 98WO-US007126.
 PA (CALJ) CALGENE LLC.
 PA (ABB) ABBOTT LAB.
 XX Knutzon D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
 PI Leonard AE;
 XX DR WPI; 1998-594582/50.
 DR P-PSDB; ANN84137.

XX New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed.

XX PS Claim 1; Fig 3A-E; 165pp; English.

XX The present sequence encodes a Mortierella alpina fatty acid delta-6 desaturase enzyme. The enzyme sequence is used in the methods of the invention. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. The present desaturase is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty acids. The enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit Platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastrointestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs. Prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and inflammatory skin disorders.

XX SQ Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

XX QY Query Match 7.5%; Score 153; DB 2; Length 1617;
 Best Local Similarity 47.9%; Pred. No. 1.7e-27;
 Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;

DB 398 GGAGACTGCTGGATATCGTCATGGCTAACAGAGAAAGGTGTATGATATTAGCCGGTGTGGAC 457
 DB 158 GCACCCCTTCCTGATGATCATCGACAAAGGTGTACGATGTCGTCCTCTGAT 217

QY 458 CACCCCTGGAGGGACGGTAATTAGCACCCTACTTGGCGGATGSCAACAGCTTTTCGCA 517
 DB 218 CATTCCGGTTGGAAAGTGTGATTCTCACGACGTTGGCAAGGACGGCACTGACGTCTTTGAC 277

QY 518 ACATTCACATCCACCTGGCGATGGAAAGCAACTCAATGACTACTACATTGGASACCTTSGCT 577
 DB 278 ACTTTTCACCCGGAGGGTGTGGAGACTCTTACGTTGGTGTATTGAC 337

QY 578 AGGGAGAGGCC-----CTTGATGAATGCTTAAGAGACTACAGAGHTATGAGAGSCC 628
 DB 338 GGAGGGGACCGCGATATCAAGAATGATGACTTTGGGCCGGAGTCCGCAAGGTGCTTAC 397

QY 629 GAGTTTGTAGAGAAGGGCTTCAAGAGTTCCAAAGGCTCTGGTCCAGACTCTG 688
 DB 398 TGTGTCAGTCTCTGGTTACTACGATCTTCCAAAGGCTACTACGCTTCAAGGTCTCG 457

QY 689 ATTAATGCGAGCTCTC-----TTTGCTGGAGCATTGGCAACTATCTGTTACGACAAGAGT 742
 DB 458 TICAAACCTCTGCATCTGGGTTCATGTGGCAAGTGGCCAAGTGGGAGACCTCG 517

QY 743 TACTGGGCTATTGGCTGGCTAGCCAGTTCATCAACAGGTCCTGGTGTGAGAACTCTTCTTT 802
 DB 518 ACCCTCGCCAACTGTCATCTGGCTTCAGGTCTCATGGTGGCAAGTGGGAGATCTTTC 637

QY 803 CTGGCCCATGATTGGCTGGCTTCATCAACAGGTCCTGGTGTGAGAACTCTTCTTT 862
 DB 578 TGGCTCAGACCTTTCGATCACAGGTCTTCAGGACCGTTCTGGGTGATCTTTC 637

QY 863 GGCTATTTGGCAATTGGCTGGCTTCAGTGGGAGGACGAGGAC 922
 DB 638 GCGGCCCTCTGGAGGTCTCGTCCAGGACGGCTTCAGGACAGGAAAGCAC 697

QY 923 AACATTCACTACTGGTCCGAATGAGTGGCAACAGTACACACTCTAGCGAAGAC 982
 DB 698 AACACTCACACGCCCAACGTCACGGGAGGATCCGACACCCACCT 757

983	ATTGATACTCTCCCCATCATTGCCCTGGAGCAAGGAAATTTCACCGTTGCCCACCGTTGAGAGCAAG	1042	XX	WO9846764-A1.
758	CTGTGACCTGGAGTGGCATGGCTTCAATATCAGCTTACATGATTCTGCCTCTATGTTCATGGCTG	817	XX	22-OCT-1998.
1043	AGAATTGGCAGTGCTTCAATATCAGCTTACATGATTCTGCCTCTATGTTCATGGCTG	1102	XX	10-APR-1998;
818	ACCCGATCTGGCTTCAATGCTGGCTTACAGACCTGGTTACTTCCCATTCTC	877	XX	98WO-US007421.
1103	CGGTACAGTTGGACTTTGGAAAGTTGCTTACATTCAAT-----	1144	PR	11-APR-1997;
878	TCGTTTGCCGTCCTGGTGGCTAACCTCTTGCTGCTAACGGTAG	937	PR	97US-00833610.
1145	-----CCTGAACTGGCAGGAAAGGGATTGATAAGAGAAGGGAAACAGTTGCT	1192	PR	97US-00834033.
938	GCCCAACAAGCCCTGGGGCGGTGGTGGCTAACGGTAG	997	PR	97US-00834655.
1193	TTTCACTACGGCTGGTTCAAGTGGCTCCATATTTCGGGGTGTGCTAAAGCCT	1252	PR	24-OCT-1997;
998	ATGCACTGGCACCTGGTACCTCGCACCATGTTCCCTGTCATCAAGGATCCTGCAACATG	1057	XX	XX
1253	CTTGGCTGGATGGTAGCAAACCTGGCTTGTGGCTGGATCTGTGTTACG	1312	PT	WPI; 1999-080739/07.
1058	CTGGGTGACTTTGGTGTGGCAAGGAACCTGGCGATCTGTGTTCTCG	1117	PT	P-PSDB; AAW95504.
1313	TTGAGTCACAAATGGAAAGGAGTTACAATGAATCG-----AAGGACTCTGTG	1360	XX	XX
1118	CTCAACCACACGGTAATGCCCTGATCTCGAAGGGAGGGCTGGATATGGATTCTTC	1177	CC	Nucleic acid construct able to express fatty acid desaturase in plants - useful in human or animal nutrition, as cosmetics and therapeutically, e.g. for restenosis, cancer and diabetes.
1361	AGAGCCCAGGTTATTACCCGTAACACCAAGGGCTGGTTCAACGATTGGTCACT	1420	CC	PT
1178	ACGAAGCAGATCATCGGGTGTGATGGTCCACCGGGTCTACTTGCCAAACTTGGCGATCTGTGTTCTCG	1237	CC	PT
1421	GGGGGACTCGACACCCAGATTGAGCATCACCTGTTCCAACATGCCAGGACAACTAC	1430	CC	PT
1238	GSTGGATTGAACTTCGATCGGGACCACCTGGTGTGTCCTTGCTGATGCCACAACTTT	1297	CC	Claim 1; Fig 3A-E; 210pp; English.
1481	CCCAAAGATCGCACCTCGAGGTGAGCATCACCTGTTGCCAAAGGGCTCGAGTAGGATAAT	1540	CC	This DNA encodes a <i>Mortierella alpina</i> delta 6 desaturase. The invention relates to a nucleic acid construct that contains at least one of the nucleotide sequences (AAK00889 to AAK00891) encoding <i>M. alpina</i> delta 6, delta 12 and delta 5 desaturases (AAW95504 to AAW95506) respectively, coupled to an expression control sequence functional in plants. Recombinant plant cells containing at least one DNA encoding a <i>M. alpina</i> fatty acid desaturase (FAD), can be used for the production of polyunsaturated fatty acid (PUFA). These recombinant cells or plants containing them are used to produce oils such as linoleic acid, arachidonic acid, gamma-gamma-linolenic acid, stearidonic acid and eicosapentaenoic acid (EPA). These plant oils are used: (i) to treat malnutrition; (ii) in infant feeding formulas, or dietary supplements or substitutes, for use in humans or animals; (iii) for treating disorders associated with inadequate consumption or production of PUFA (or their metabolites such as prostaglandins), e.g. restenosis after angioplasty, inflammation, AIDS, rheumatooid arthritis, psoriasis, osteoporosis, cancer, eczema; (iv) as cosmetics, and (v) as animal feeds. Fragments of the DNA are used as probes to isolate related coding sequences. Recombinant plants can produce high yields of PUFA, since new pathways can be created and unwanted ones suppressed. Plants can be engineered to express oils of particular PUFA composition, e.g. one similar to that in human milk, and product recovery is simpler than with e.g. fish.
1298	TCAAAGATCCAGCTGGTGTGAAAGTACAATGTGTCGATGGCTGATAACCACACC	1357	CC	XX
1541	GTCTCCGTCGTTGGCTCTGTGCGGTGAGGCTCAAGGAAATTGCTGATGAA	1600	CC	SQ
1358	ACCGGTATGATCGAGGGAAACTGCAAGGGTCTGGTGTGAAAGGAGGTCTCCAGGGCT	1417	CC	Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;
1601	GCGTCAATTGGCTTCAGCTCACTAAGAAA	1631	CC	Query Match 7.5%; Score 153; DB 2; Length 1617;
1418	GCCTCCAAAGATGGTAAAGGCACTAAAGAAA	1448	CC	Best Local Similarity 47.9%; Pred. No. 1..7e-27;
			Matches 0; Mismatches 615; Indels 57; Gaps 4	Matches 619; Conservative
				Qy 398 GGAGACTGCTGGATGATCGTCAAAGAGAAAGGAACTTGGCTGGAGGAGAC
				Db 158 GCACCCCTCTGATGATCATCGACAAACAAGGTGTGATTCGATGCTCCCTGAT
				Qy 458 CACCTGGAGGGACGGTAACTTGGACCTTGTGCTGGCTGGAGGCTGGAGGAGAC
				Db 218 CATCCCGTGGAGGTGTGATTCACGGCAGTGTGCTGGCAAGGACGGCAACTG
				Qy 518 ACATTCCATCCACCTGCCATGGAGGAACCTCAATGACTACTACATTGGAGACCTTGCT
				Db 278 ACTTTTACCCGAGGCTGGAGACTCTGGCAACCTTACGGTGTGATATTGAC
				Qy 578 AGGGAAAGAGCCC-----CTTGATGAATTGGCTAAAGACTACAGAGATATGAGAGCC
				Db 338 GAGAGGGACCGGATATCAAGAATGACTTGGCTGGAGGCTCGCAAGGCTGCTACC
				Key 71..1443 /*tag= a /product= "delta 6 desaturase"
				CDS 397

Search completed: June 18, 2004, 22:56:11
 Job time : 829 secs

QY	629	GAGTTGTTAGAGAAGGCCCTTCAAGAGTTCCAAGGCCTGGCTTCAGACTCTG	688
Db	398	TGTTCAGTCTCTGGTTACTACGATTCCAAGGCATACTACGCTCAAGGCTCG	457
QY	689	ATTAATCAGCTCTC-----TTTGCTGCCGAGCATTCGACTATCTGTTACGACAAGGT	742
Db	458	TTCAACCTCTGCATCTGGGTRTCGACGGTCAATGGCCAAAGGGCCAGACCTCG	517
QY	743	TACTGGGTATTGCTGCTGCCAGGTTGAIGGGTCTCTCGTCCAACAGTGGATGG	802
Db	518	ACCTCGCCAACGTGCTCTCGCTGGCTTGCGCTTGGTCTGAGGATGGATGG	577
QY	803	CTTGCCCATGATTCTTCATCACACGGTCTTGAAGACCGTACCCGAACTCCCTCTT	862
Db	578	TGGCTCACGACTTTGCTACCCAGGTCTCCAGGACCGTTCTGGGTRGATCTTTC	637
QY	863	GGCTATTGTTGGCAATTGGCTGGCTTGGCTTAGTGTATCGTGGAGGACAGCAC	922
Db	638	GGGCCCTCTGGAGGTGCTCCAGGGCTCTCGTCTCGTGGAGAACAGCAC	697
QY	923	AACATTCACTCATACTGCTCCGAATGAGTSGACGAACAGTACACACCTCTGACGAAGAC	982
Db	698	AACACTAACCGCCGCCCAACGTCAGTCCAGGGAGATCCCGACATTGACACCCACCT	757
QY	983	ATTGATACTCTCCCATCATTCATTGGAGCAAGGAATTGGCACCGTTGAGGCAAG	1042
Db	758	CTGTTGACCTGGAGTSAGCATGTTGGAGATGGTCTCGGATGTCAGATGGAGCTG	817
QY	1043	AAGAATTTCGAGTCTCGATCTCGATTCATGATTCTGCCTCTATTGTTCATGGCC	1102
Db	818	ACCGCGATCTGGTGGGTTCATGGTCTCCGAACCGAACCTGGTTTACTTCCTTC	877
QY	1103	C3GTACAGTTGGACTTTGGAAATTGGCTCTTCACATTCAAT-----	1144
Db	878	TGTTTGGCCGTCCTGGCCTCCAGTCCATTCTTGTGCTGCTAACGSTDAG	937
QY	1145	-----CCTGATTGAGCACGCCAGGGATGGCATGATAGAAGAAACAGTGCT	1192
Db	938	GCACAGCCCTCGGGCGCGTGTGCGCCATCTCGTCTCTGCTGAGCTGCTGCG	997
QY	1193	TTTCACTACGCCCTGGTTCAAGTGGGTTCCATATTGCGGGTGTGCTTAAGCCT	1252
Db	998	ATGCACTGGACCTGGTACCTGCCACCATGTTCCATTCTGCTGATGGTCTCG	1057
QY	1253	CTTGCTGGATGGTGGCAACTGAGCTGGCCGGTTGCTGCTGAGCTGCTGCG	1312
Db	1058	CTGGTGTACTTCTGGTGTGATCTCGAAGGGTGTGGAAACCTGGTGGATGGTCTC	1117
QY	1313	TGAGTCACATGGAAAGGGTTTACAATGAACTG-----AAGGACTTCGTC	1360
Db	1118	CTCAACCACAAAGGTATGCGCTGTGATCTCGAAGGGAGGGGGTGTGATGGATTCTTC	1177
QY	1361	AGAGCCCAGGTATTACACCGTAAACACCAAGCGAGGCTGGTTCAACGATGGTCACT	1420
Db	1178	ACGAAGGAGATCATACGGGTOGTGATGTCACCGGGCTTACCTGGCTACG	1237
QY	1421	GGGGGACTCGACACCCAGATTGAGCATCACCTGTTCCAACAATGCCAGGACAAC	1480
Db	1238	GGTGGATGAACTATGAGTCAGATCGAGGACCCACTGTTGGCTCGCACAAC	1297
QY	1481	CCCAAGATCGCACCTCAGGTCAGGTGCTGGCTCTTGCAAGAAGGCACGGCTCG	1540
Db	1298	TCAAGATCCAGGCTCTGGCTCTGTCAGACCCCTGTGAAARAGTACATGTGATGAA	1357
QY	1541	GTCTCCGGTCTGGCTCTGTCGGGTGTGAAAGGCGCTCAAGGAAATTGGTGTGATGAA	1600
Db	1358	ACCGGATGAGGGAAACTGAGGGTCTTACGAGGTTCTGGCTCCAGGCTCAAGGCT	1417
QY	1601	GCCTCAATTGGCTCTACGCTCACTARGAAA	1631
Db	1418	GCCTCCAAGATGGGTAAGGGCACTAAAAAA	1448

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
 Run on: June 18, 2004, 21:42:16 ; Search time 156 Seconds
 (without alignments)
 7257.050 Million cell updates/sec

Title: US-09-980-468-1
 Perfect score: 2040
 Sequence: 1 ctccaggcaggctcgtatgaa.....aaaaaaa 2040

Scoring table: IDENTITY_NUC
 GapO 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents_NA:
 1: /cgmn2_6/pctodata/2/ina/5A_COMB.seq:
 2: /cgmn2_6/pctodata/2/ina/5B_COMB.seq:
 3: /cgmn2_6/pctodata/2/ina/6A_COMB.seq:
 4: /cgmn2_6/pctodata/2/ina/6B_COMB.seq:
 5: /cgmn2_6/pctodata/2/ina/PCITS_COMB.seq:
 6: /cgmn2_6/pctodata/2/ina/backfiles1.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	153	7.5	1617	2 US-08-834-655-1	Sequence 1, Appli
2	153	7.5	1617	3 US-08-834-653A-1	Sequence 1, Appli
3	153	7.5	1617	3 US-09-363-514-1	Sequence 1, Appli
4	153	7.5	1617	4 US-09-363-526-1	Sequence 1, Appli
5	153	7.5	1617	4 US-09-330-235-17	Sequence 17, Appli
6	96	4.7	1686	4 US-09-439-261-6	Sequence 6, Appli
7	96	4.7	1686	4 US-09-227-613-6	Sequence 6, Appli
8	96	4.7	1843	4 US-09-439-261-7	Sequence 7, Appli
9	96	4.7	1843	4 US-09-227-613-7	Sequence 7, Appli
10	96	4.7	2257	4 US-09-439-261-8	Sequence 8, Appli
11	96	4.7	2257	4 US-09-227-613-8	Sequence 8, Appli
12	96	4.7	2540	4 US-09-023-655-295	Sequence 295, Appli
13	90.2	4.4	1362	4 US-C9-769-863-13	Sequence 13, Appli
14	87.6	4.3	1717	4 US-09-048-888-2	Sequence 2, Appli
15	87.2	4.3	1684	2 US-08-B31-570-1	Sequence 1, Appli
16	87.2	4.3	1684	2 US-08-831-575-1	Sequence 1, Appli
17	87.2	4.3	1685	1 US-08-366-79-4	Sequence 4, Appli
18	87.2	4.3	1685	1 US-08-789-936-4	Sequence 4, Appli
19	87.2	4.3	1685	4 US-08-934-254-4	Sequence 4, Appli
20	87.2	4.3	1685	4 US-09-685-75-4	Sequence 4, Appli
21	80.4	3.9	1478	4 US-09-148-545-63	Sequence 63, Appli
22	80.4	3.9	2016	4 US-09-148-545-119	Sequence 119, Appli
C 23	79.2	3.9	347	4 US-09-702-705-355	Sequence 355, App
C 24	79.2	3.9	347	4 US-09-736-457-355	Sequence 355, App
C 25	79.2	3.9	347	4 US-09-614-124B-355	Sequence 355, App
C 26	79.2	3.9	347	4 US-09-671-325-355	Sequence 355, App
C 27	79.2	3.9	347	4 US-09-589-184-355	Sequence 355, App

ALIGNMENTS

28	79	3.9	449	4 US-09-439-261-38
29	79	3.9	449	4 US-09-227-613-37
30	79	3.9	473	4 US-09-439-261-37
31	79	3.9	473	4 US-09-227-613-36
32	79	3.9	655	4 US-09-439-261-3
33	79	3.9	655	4 US-09-227-613-3
34	79	3.9	864	4 US-09-439-261-12
35	79	3.9	864	4 US-09-227-613-13
36	79	3.9	1335	4 US-09-439-261-1
37	79	3.9	1335	4 US-09-227-613-1
C 42	50.8	2.5	19513	4 US-10-204-708-39
C 43	50.6	2.5	593	4 US-09-904-615-59
C 44	50.4	2.5	1413	4 US-09-769-863-19
45	49.8	2.4	266	4 US-09-313-294A-3256

RESULT 1				
US-08-834-655-1				
; Sequence 1, Application US/08834655				
; Patent No. 5968309				
GENERAL INFORMATION:				
; APPLICANT: KNUTZON, DEBORAH				
; APPLICANT: MURKERJI, PRADIP				
; APPLICANT: HUANG, YUNG-SHENG				
; APPLICANT: THURMOND, JENNIFER				
; APPLICANT: CHAUDHARY, SUNITA				
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS				
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS				
; NUMBER OF SEQUENCES: 18				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.				
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039				
; CITY: PALO ALTO				
; STATE: CA				
; COUNTRY: USA				
; ZIP: 94306				
COMPUTER READABLE FORM:				
; MEDIUM TYPE: Floppy disk				
; COMPUTER: IBM PC compatible				
; OPERATING SYSTEM: PC-DOS/MS-DOS				
; SOFTWARE: PatentIn Release #1.0, version #1.3.0				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/08/834, 655				
; FILING DATE: 11-APR-1997				
; CLASSIFICATION: 435				
; ATTORNEY/AGENT INFORMATION:				
; NAME: RAE-VENTER, BARBARA				
; REGISTRATION NUMBER: 32,750				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: (650) 328-4400				
; TELEFAX: (650) 328-4477				
; INFORMATION FOR SEQ ID NO: 1:				
; SEQUENCE CHARACTERISTICS:				
; LENGTH: 1617 base pairs				
; TYPE: nucleic acid				
; STRANDEDNESS: single				
; TOPOLOGY: linear				
; MOLECULE TYPE: other nucleic acid				
; US-08-834-655-1				
; Score 153; DB 2;				
; Pred. No. 3.7e-34;				
; Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;				

Qy	398	GGAGACTGCTGGATCAAGAGAAGGTGATGCGTTTGGGGACCGAC 457	Db	1238	GTTGGATTGAACATAAGATCGAGCACCCTGTCGCTGCCAACCTT 1297
Db	158	GCACCCCTCTTGATGATCATCGACAACAGGTGACATGGCTGAT 217	Qy	1481	CCAAAGATCGCACCTCAGGTGAGGCTCTTGCAGAGTCGAGTAAT 1540
Qy	458	CACCTGGAGGGACCGTAAATTAGCACCTTACTTTGGGGATGGCACAGACCTTTCGCA 517	Db	1298	TCAAAGATCCAGCTGCGAACCTGCAAAAGTACAATGCGATAACCACCC 1357
Db	218	CATCCGGTGGAAAGTGTGATTCTCACGGCACGTTGGCAAGGACGGCACTGACCTTGCAC 277	Qy	1541	GTCTCCGTCGGTTGGTGCCTCTGCGGTTGTAAGGGCTCAAGGAATTGGTGTGAA 2600
Qy	518	ACATTCCATCCACCTGCCGATGGAAGGCHAATCAATGACTACATTGGGACCTTGT 577	Db	1358	ACCGGTATGATCGAGGGAAACTGCAGAGGTCTTAGCCGTTAGCCAAGGGCT 1417
Db	278	ACTTTCACCCGAGGACTGCTGGAGACTCTGCCAACITTAACGGTGGATATTGAC 337	Qy	1601	GGTCAATTGCGCTTACGCTCACTAGAAA 1631
Qy	578	AGGGAAAGGCCCTTCTTGATGAAAGACTACAGAGATATGAGGCC 628	Db	1418	GCCTCCAAGATGGGTAGGGCAGTAAAAAA 1448
Db	338	GAGGGACCGCGATAATCAAGGAATGATGACTTGGGGAGCTGGCAAGCTGGTACCC 397			
Qy	629	SAGTTGTTAGAGAAGGGCTTTCAAGAGTCCAAAGSCTTCTCTGCTTCAAGACTCTG 688			
Db	398	TTTTCAGTCAGTCTCTTGGTACACGATTCCAAAGSCATACTAACGCTTCAAGGGTCTCG 457			
Qy	689	ATTAATGCGAGCTCTC-----TTTGCTGGGATTGGCACTATCTGTTACGACAGAGT 742			
Db	458	TTCAACCTCTGCATCTGGGTTGTCGACGGTCAATTGGCAAGGGCAGACCTCG 517			
Qy	743	TACTGGCTTATGGTGTGGTCAAGCCAGTTGATGGGTCTTCTGTCACAGTGTGGATGG 802			
Db	518	ACCTCTGCCAACGGTCTCTGGGTCTGGCTTGGGTTGGGGATGGGGATGGGGATGG 577			
Qy	803	CTTGCCTCAGATTCTCATCAACAGGTCTTGAGAACCGTACCCGGAACCTCCCTTCTT 862			
Db	578	TTGGCTTAACGACTTTGGCATACAGGTCTTCGGGTCTGGGTGATCTTTC 637			
Qy	863	GGCTTATTGTTGGCAATTGGGTCTGGTTAGTSTATCATGGTGGAGAACGGAC 922			
Db	638	GGGCCTCTGGGAGGTGGCATACAGGTCTGGGTCTGGGTGGAAAGGACAGGGCAC 697			
Qy	923	AACATTCCATCATACTGCTCCGAATTGGGTCTGGTTAGTSTATCATGGTGGAGAACAGAC 982			
Db	698	AAACACTTACACACGCGCCCCAACGTCCACGGGAGATCCCACATTGACACCCACCT 757			
Qy	983	ATTGATAACTCTCCCATCATGGGTCTGGCTTGGCTTGGGCTTGGGCTTGGGCTTGGG 1042			
Db	758	CTGGTGGCTGGAGGTGGCATACAGGTCTGGGTGGGAGATGGTCCAGATGGAGGGCTG 817			
Qy	1043	AGAATTGGGACTTGGGACTTGGCTCAATATCAGCACTCATGATTCTGCTCTCTATTGGTCTATGGGCC 1102			
Db	818	ACCGGCGATGGTGGCTCTCATGGTCTGGCTTCTGCTTACCTGGGCTTGGCTTC 877			
Qy	1103	CGGTACAGTTGGACTTTGGGAAGTGGCTTCAATTCATTCACATTCAAT----- 1144			
Db	878	TGTTTGGCCCGTCTCTCTGGTCCATTCTGGTCTGGCTGCTAACGGTCAG 937			
Qy	1145	-----CTGTATTGGGACTTGGGAGGTGGATGGGATTTGATAGAGAAACAGTTGCT 1192			
Db	938	GCCCAACAGCCCTGGGGCTGGCTGCCCACATCTGGTCTGGCTGCTGGATGGTCTCG 1117			
Qy	1193	TTTCACCTACGGCTGGTCACTGGTGGCTCCATATTGGCTGCTAACGGTCAAGCT 1252			
Db	998	ATGCACTGGACCTGGTACCTGCCACCATGTTCTGCAAGGATCCGGTCAACATG 1057			
Qy	1253	CTTGCCTGGATGGTAGCAACTGAGCTGGCTGGCGGTTGGGATTGTTGTTACG 1312			
Db	1058	CTGGCTGACTTTGGTGGGGCTGGCTGGCTGGGGAAACTCTGGTGGGATGGTCTCG 1363			
Qy	1313	TGAGTCAATGGAAAGGGGTTACATGAATGATGCACTGGCTGGCTGGCTGGCTGG 1363			
Db	1118	CTCAACACAAACGGTATGCGCTGGTGTGATCTGGCTGGCTGGCTGGCTGGCTGG 1177			
Qy	1361	AGAGCCAGGTATTACCCCGTAACACCAAGGGAAGGGCTGGTCAACGATGGTTCACT 1420			
Db	1178	ACGAAGCAGATCATCACGGGTGCTGATGTTGGCTGGCTGGCTGGCTGGCTGG 1237			
Qy	1421	GGGGAACTCGACACCCAGATTGAGCATCACCTGTTCCAACAAATGCCAGGCAACTAC 1480			
Db	218	CATCCGGTGGAAAGTGGTCACTCACGGCACSTGGCAAGGGACTTGAC 277			

RESULT 2

US-28-834-033A-1

; Sequence 1, Application US/0BB34033A

; Patent No. 6075183

; GENERAL INFORMATION:

; APPLICANT: KNUTZON, DEBORAH

; APPLICANT: MUKERJI, PRADIP

; APPLICANT: HUANG, YUNG-SHENG

; APPLICANT: THURMOND, JENNIFER

; APPLICANT: CHAUDHARY, SUNITA

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS

; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.

; STREET: 2001 FERRY BUILDING

; CITY: SAN FRANCISCO

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WORDPERFECT 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/834,033A

; FILING DATE: 11-APR-1997

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: WARD, MICHAEL R.

; REGISTRATION NUMBER: 38,651

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 433-4150

; TELEFAX: (415) 433-8716

; TELEX: N/A

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1617 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-834-033A-1

; Query Match 7.5%; Score 153; DB 3; Length 1617;
; Best Local Similarity 47.9%; Pred. No. 3.7e-34;

; Matches 619; Conservation 0; Mismatches 615; Indels 57; Gaps 4;

; Qy 398 GGAGACTGGCTGGATGATCGCTAACAGAGAAGGGCTTATGGCGTTGGGAGCGAC 457

; Db 158 GCACCCCTCTTGATGATCATCGACAACAGGTGACATGGCTGAT 217

; Qy 1118 AGAGCCAGGTATTACCCCGTAACACCAAGGGAAGGGCTGGTCAACGATGGTTCACT 1420

; Db 1178 ATGCACTGGACCTGGTACCTGCCACCATGTTCTGCAAGGATCCGGTCAACATG 1237

; Qy 458 ACGAAGCAGATCATCACGGGTGCTGATGTTGGCTGGTCAACGTTGGTCACT 1480

; Db 218 CATCCGGTGGAAAGTGGTCACTCACGGCACSTGGCAAGGGACTTGAC 277

QY 518 ACATCCATCCACCTGCCAAGCAACTCAAATGACTACTCATGGAGACCTTGGCT 577
 Db 278 ACTTTTCAACCCGAGGTCTGGACTCTTGGCTGATTGATATTGAC 337
 QY 578 AGGAAGAGCCC-----CTTGATGAATTGCTTAAGACTAACAGAGATAATGAGGCC 628
 Db 338 GAGAGCAGCGATACTCAAGATGATGACTTTCGGCCGAGSTCGGCTGTAAC 397

QY 629 GAGTTGTTAGAGAAGGGCTTTCAAGAGTTCCAAGGCCCTGGTTCTGACTCTG 688
 Db 398 TTGTTCCAGTCTTGGTTACTACGATTCCAAAGCATACTACGCCTTCAAGGTCG 457

QY 689 ATTAAATGCGCTCTC-----TTTGCTGGAGCAATTGGACTATCTGGTACAGGT 742
 Db 458 TTCAACCTCTGCACTGGGTITGTGACGGTCAATTGGCCRAAGTGGGCTGAGACCTCG 517

QY 743 TACTGGGCTTATTGTTGCAAGCCAGTTGATGGGTCTCTTCGTTCAACAGTGGATGG 802
 Db 518 ACCCTCGCCAAACGTTGCTCTCGGTGCTGGCTGTTGGTCTGTTGGGATGG 577

QY 803 CTTGCCCATGATTTCCTTCATCAACAGGTCTTGGAAACCGTACCGGAACCTTCTT 862
 Db 578 TGGCTCACGACTTTGCACTACCAGGTCTTCAGGTTCCAGGTTCTGGGTRGATCTTC 637

QY 863 GGCTATTGTTGGCAATTGGCTTAGTGTATCATGGTGGAGGACGAGCAC 922
 Db 638 GGCGCCCTTGGAGGTGCTGCCAGGGCTCTCGTGTGGAAAGACAAGCAC 697

QY 923 AACATTCACTACATGCTCCATCATGGTGGACTACACACCTCTAGACGGAGAC 982
 Db 698 AACACTCCACGCCAACGGCCAAACGTCCACGGGAGATCCGCACCCACCT 757

QY 983 ATTGATATCTCCCATCATGGCTGGAGTCTGGCACCGTTGAGGCCAG 1042
 Db 758 CTGTTGACCTGGAGTGAGCTGGATGTTCTGGATGTUCCAGATGGAGGCTG 817

QY 1043 AGAATTGGGAGTCTCAATATCAGGACTACATGATTCCTGGCTCATGGCC 1102
 Db 818 ACCCGCATGTTGCTTCATGGTCTCTGAACCCGAACTGGTTTACTTCCCATTCTC 877

QY 1103 CGGTACAGTTGGACTTTGGM37-TGCTTCACATCAAT-----
 Db 878 TCGGTTGCCCGTCTCTGGCTCCAGTCCATTCTGGCTGCCTAACGGTCA 937

QY 1145 -----CCTGATTGAGCACGACCAAGGGATGATAGAGAAGGGAAACAGTTGCT 1192
 Db 938 GCCCACAAAGCCCTGGGCGGCGTGTGCCCATCTCGTGGCTGCTGG 997

QY 1193 TTTCACTACGCCCTGGTTCAGTGGCTGCCATATTTGCCGGTGTGCTTAAGCT 1252
 Db 998 ATGCACTGGACCTGGTACCTGCCACCATGTTCTGTCACTCAAGGATCCGGTCAACATG 1057

QY 1253 CTTSGCTGGATGGTAGCAACTGAGCTGGTGGGATTGCTGTTGGATTGCTG 1312
 Db 1058 CTGGTGTACTTTGGTGTGGGGAAACTGTGGGATGCTGGCTGGTCTCG 1117

QY 1313 TTGAGTCACAATGGAAGGGTTACATGAAATGAGTGGCTGGCTGGCTGG 1360
 Db 1118 CTCAACCAACGGATGCTGGTGTGATCTGGAGGGAGGGGGTGTGCTTC 1177

QY 1361 AGAGCCCAAGTTATTACCAACCGTAAACCCGAGCTGGTCAACGATGGTCACT 1420
 Db 1178 ACGAAGCAGATCATACGGGTCTGTGATGTCACCTGCAACTGTTCACT 1237

QY 1421 GGGGACTCGCACCCAGATTGAGCATCACCTGTTCAACAAATGCCAGGACACATAC 1480
 Db 1238 GGTGGATTGAACATCAGATGGACCAACTGGTCCCTTGATGGCTGGCTGG 577

QY 1481 CCCAAGATGGCACCTCAGGTGAGGGCTCTTGGCAAGAACGGCTGAGTACATA 1297
 Db 1298 TCAAAGATCCAGCCTGGAGACCTCTGCAAAAAGTACAAATGTCGATACACC 1357

QY 1541 GTCTCCGTCGTTGGCTCTGGCTGGGCTCAAGGAATTGGCTGATGAA 1600
 Db 1358 ACCGGTATACTGAGGAACCTGAGGCTCTGGCTGCTTAAGGCTCCAAAGGCT 1417

RESULT 3
 US-09-363-574-1
 ; Sequence 1, Application US/09363574
 ; Patent No. 6136574
 ; GENERAL INFORMATION:
 ; APPLICANT: KNUTZON, DEBORAH
 ; APPLICANT: MURKERJI, PRADIP
 ; APPLICANT: HUANG, YUNG-SHENG
 ; APPLICANT: THURMOND, JENNIFER
 ; APPLICANT: CHAUDHARY, SUNITA
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
 ; STREET: 2001 FERRY BUILDING
 ; CITY: SAN FRANCISCO
 ; STATE: CA
 ; ZIP: 94111
 ; COUNTRY: USA
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/363,574
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: WARD, MICHAEL R.
 ; REGISTRATION NUMBER: 38,651
 ; REFERENCE/DOCKET NUMBER: CGAB-202 USA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 433-4150
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1617 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 JS-09-363-574-1
 Query Match 7-54; Score 153; DB 3; Length 1617;
 Best Local Similarity 47.94%; Pred. No. 3.7e-34;
 Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4;
 QY 398 GGAGACTGCTGGATGATCTGGTCAAAGAGAACGGTGTATGATATTGCCGTTGGGACG 457
 Db 158 GCACCCCTCTGTGATCATGGACAAACGGTGTACATGCCGAGTTCGTCCTCTGAT 217
 QY 458 CACCTGGAGGGACGGTAATTAGCACCTACTTGGGGATGGCACAGACGTTTCGCA 517
 Db 218 CATCCCCGGGGAAAGTGTGATTCTACGCGAGCTTCACGGCAAGGACGGCACTGACGTTGAC 277
 QY 518 ACATCCATCCACCTGCCATGGACCAACTGGTCCCTTGATGGCTGGCTGG 577
 Db 278 ACTTTTCACCCCGGGGCTGCTGGGAGACTCTTGGCAACTTTACGTTGGTATATTGAC 337
 QY 578 AGGAAGAGGCC-----CTTGTGAAATTGCTTAAGGACTACAGAGATAGAGGCC 628

RESULT 4
 US-09-363-526-1
 Sequence 1, Application US/09363526
 Patent No. 6410288
 GENERAL INFORMATION:
 APPLICANT: KNUTZON, DEBORAH
 APPLICANT: MURKERJI, PRADIP
 APPLICANT: HUANG, YUNG-SHENG
 APPLICANT: THURMOND, JENNIFER
 APPLICANT: CHAUDHARY, SUNITA
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
 TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: LIMBACH AND LIMBACH L.L.P.
 STREET: 2001 FERRY BUILDING
 CITY: SAN FRANCISCO
 STATE: CA
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/363,526
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: WARD, MICHAEL R.
 REGISTRATION NUMBER: 38,651
 REFERENCE/DOCKET NUMBER: CGAB-201 USA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 433-4150
 TELEFAX: (415) 433-8716
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1617 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 US-09-363-526-1
 Query Match 7.5%; Score 153; DB 4; Length 1617;
 Best Local Similarity 47.9%; Pred. No. 3.7e-34;
 Matches 619; Conservative 0; Mismatches 615; Indels 57; Gaps 4
 QY 398 GGAGACTGCTGGATGATCGTCAAAGAGAAGGTGTATGATAATTAGCCGTTTGCGGACGCC 457
 DB 158 GCACCCCTTCCTTGATGATCATGACAAAGGTGTACGATGTCGGGGAGTTTCGCA 217
 QY 458 CACCCCTGGAGGGACGGTANTTAGCACCCTACTTGGGGGATGGCACAGAGTTTCGCA 517
 DB 218 CATCCCCTGGAAAGTGTGATTCACGCACGTGGCAAGGACGGCACTGACTCTTTGAC 277
 QY 518 ACATTCATCCACCTGCCATGGAAAGCACTCAATGGAGACTACTACATTGGAGACCTTGTGCT 577
 DB 278 ACTTTTCACCCCAGGGCTTGGAGACTCTTACGTTGGGAGACTCTTACGTTGGATATTGAC 337
 QY 578 AGGGAAGAGCCC-----CTTGATGAATTGCTTAAGAGATAATGAGAGGCC 628
 DB 338 GAGAGGGAACGGCGATATCAAGAATGACTTGGCCGGAGGTGGCTCTGCTTCAAGGTCTCG 397
 QY 629 GAGTTGGTAGAGAAGGGCTTCAAGAGTTCAAGAGCTTCTGCTTCAAGGCAACTACAGCTG 688
 DB 398 TTGTTCAAGTGGCTCTGGTTACTACAGCTTCAAGGCAACTACAGCTTCAAGGCAACTACAGCTG 457
 QY 689 ATTATATGCAAGTGGCTCTGGTTACTACAGCTTCAAGGCAACTACAGCTTCAAGGCAACTACAGCTG 742

APPLICANT: Knutzon, Debbie
 TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
 FILE REFERENCE: MOCO_156_00US
 CURRENT APPLICATION NUMBER: US/09/330,235
 CURRENT FILING DATE: 1999-06-10
 PRIOR APPLICATION NUMBER: 60/089,043
 PRIOR FILING DATE: 1998-06-12
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 17
 LENGTH: 1617
 TYPE: DNA
 ORGANISM: Mortierella alpina
 US-09-330-235-17

	Query Match	Match	Score	DB	Length
QY	923 AACATTCATCATACTGOTCCGAATGGCTGGGGCTTCTCGTCTCTAGACGAAAGAC	7.5%	153	4	1617;
Db	638 GGCGCCTTCTGGGAGGTGTCGCCAGGGCTTCGTTGGAAAGGACAAGCAC	7	Best Local Similarity	4.7%	Length 1617;
Db	698 AACACTCCAACGGCGGGATCCCAGACATTGACACCCACCT	0	Mismatches	3.7e-34;	
Db	758 CTGGTGACTCTGGAGTAGCATGGTTGGAGATGGTCCTGGATGGAGGTG	4	Matches	619;	
QY	983 ATTGATACTCTCCCATCATGGCTGGGAAAGGAAATTGGCACCCGTTGAGAGCAAG	4.5	Conservative	4.7e-34;	
Db	818 ACCCGCATGTTGGCTCGCTTCATGGCTGGCTGGAGCTGGTCCATTCTC	57	Indels	57;	
QY	1043 AGAATTGGGAGTTCAATATCAGGACTACATGATGTTCTATGTTCATGGGC	4.5	Gaps	4;	
Db	878 TCGTTGCCCTGCTCCCTGGCTGGCTGGCTTAACGGTCAG	57	QY	398 GGAGACTGGTGGATGATCGTCAGAGAAAGGTGTATGATATTAGCCGTTTTCGGACGAC	4.5
Db	938 GCCCCACAAGGCCCTGGCTGGCGCCATCTCGTGGCTGGCTGGCG	57	Db	158 GCACCCCTTCATGGATCATGACAACAAAGGTGTACGATGTCGGCCCTGT	57
QY	1103 CGGTACAGTTGGGACTTTGGAAAGTTGCTCTTCACATCAAT	4.5	QY	458 CACCCTGGAGGGACGCTTATTAGCACCTACTTGGGGGATGGCACAGCTTTTCGCA	517
Db	998 ATGCACTGACCTGGTACCTGGCCACCATGTTCTGGTCAAGGATGGCTGGCG	57	Db	218 CATCCCGGGTGGAAAGTGTGATTCTCACGCACGGTCTTTGAC	217
QY	1145 -----CCTGATTGAGCACGACCAAGGGATGATAAGAAGGAAACAGTTGCT	4.5	QY	518 ACATTCCATCCACCTGGGACAACTCAATGACTACTACATTTGGAGACCTTGCT	577
Db	1058 CGGGTGTACTTTGGTGTGGCGAAACTGTTCCATTTGGCTGGTCTGGCG	57	Db	278 ACTTTTCAACCCGAGGACTGGAGACTCTGGGAGACTTACACTGGCTGATATTGAC	337
QY	1193 TTTCACTAGCCTGGTCACTGGCTGGCTGGCTTAACGGCTAG	4.5	QY	578 AGGAAAGAGCCC-----CTTGATGAAATTGCTTAAGAAGTACAGAGATATGAGAGCC	628
Db	1118 CTCAACCACAAACGGTATGGCTGCTGGTCAAGGATGGCTGGTCTTC	57	Db	338 GAGAGGGACCGCGATATCAAGAATGATGACTTGGGCCGAGGTGGCAAGGTCG	397
QY	1253 CCTGGTGTGGATGGTACACTGAGCTGGTGGGGTTGGTGTGGATTC	4.5	QY	629 GAGTGTGAGAGAAGGGCTTTCAAGAGFTTCACAGGCTGGTCCCTGCTTCAAGACTCTG	628
Db	1118 CTCAACCACAAACGGTATGGCTGCTGGTCAAGGATGGCTGGTCTTC	57	Db	398 TTGTTCCAGTCTCTGGTTACTACGATTCATTCCAAAGGCTAATCTGGCTTC	457
QY	1313 TTGAGTCACAATGGAAAGGAGTTTACAATGAAATCG-----AAGGACTTCG	4.5	QY	689 ATTAATGGAGCTC-----TTTGTGCTGGCAGGCTT3CGACTATCTGTTACGACAAGAGT	742
Db	1118 CTCAACCACAAACGGTATGGCTGCTGGTCAAGGAGGGGGTCTTC	57	Db	458 TCAACCTCTGCATCTGGGGTTGGTGCAC3GGCATTTGGCTGCAAGTGGGCCAGAC	517
QY	1361 AGAGCCAGGTTTACACCCGTAACACCAAGGGCTGGCTCAAGGTTTCACT	4.5	QY	743 TACTGGGCTTATTGGCTCTAGCCAGTTGCTTCAACAGTGTGGATGG	802
Db	1178 ACGGAAGCAGATCATCACGGCTGGCTCAACGGCTGGCTGGATCTTC	57	Db	518 ACCTCGCCAAACGGTCTCGGTGCTGGCTTGGCTGCACTGGGGATGG	577
QY	1421 GGGGGAACCTCGACACCAGATTGAGCATCACCTGTTGATGTCCACCGGGCTCAACAAATG	4.5	QY	803 CTGCCCCATGATTTCCTCATCACGGCTTGTGCTTCAACAGTCTCTCTT	862
Db	1238 GGTGGATTGAACTATCAGATCGAGCACCACTGTTCTGGTCACTT	57	Db	578 TGGCTCAGGACTTTTGATCACAGGCTTCTGGCTGCTGGCTGCACTCTTC	637
QY	1481 CCCAAGATGCACCTCAGGTGGGGCTCTTGCAGAACGGCCCTCGAGTACGATAAT	4.5	QY	863 GGCTATTGGCTGGCAAATTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG	922
Db	1298 TCAAAGATCCAGCCTGGCTGAGACCCCTGCAAAAAGTACAATGTCGATACCAC	57	Db	638 GGCGCCTTCCTGGAGGTGTCTGCAGGGCTCTGGCTGGCTGGCTGG	697
QY	1541 GTCTCCGTTGGCTGGCTCTGGCTGGCTCAAGGAATTGCTGATGAA	4.5	QY	923 AACATTCACTACACTGGCTCCGAAATGACTACACACTCTAGACGAAGAC	982
Db	1358 ACCGGTATGATCGAGGGAAACTSCAGAGGTCTCGATCCAGGTTCTCAAGGCT	57	Db	698 AACACTCACACGGCCACGGCTTCAACGGCTGCTGGCTGGCTGGCTGG	757
QY	1601 GCGTCATTGGCTTACGGCTCACTAAGAA1631	4.5	QY	983 ATGATACTCTCCCATCATGGCAAGGAAATTGGCTCATGGCC	1042
Db	1418 GCCTCCAAAGATGGTAAAGGAAACGGTAAAGAAAA1448	57	Db	758 CTGTTGACCTGGAGTGTGCTGGCTTCACTGCTGGCTGGCTGGCTGG	817
QY	1145 -----CCTGTTGGCTCTCTCTCTGGCTGGCTTCAACGGTCAAGGTCG	5	QY	1103 CGGTACAGTGGACTTTGGCTCTCATGGTCTGGCTCATGGCC	1102
Db	878 TCGTTGCCGGTCTCTCTGGCTGGCTTCACTGCTGGCTGGCTGGCTGG	57	Db	818 ACCGGCATGTTGGCTGGCTTCACTGCTGGCTGGCTGGCTGGCTGG	877

RESULT 5
 US-09-330-235-17
 ; Sequence 17, Application US/09330235
 ; Patent No. 6459018
 ; GENERAL INFORMATION:

938 GCCCACAGCCCTGGGCGGTGCCCATCTGGTGGCTGAGCGCTGGTGGCG 997
 1193 TTTCACATACGCCTGGTTCAAGTGGCTGCGTTCCATTATTTGCCCTTAAGCCT 1252
 QY 510 GACTGGTTCAAGTGGACACCTTAACCTCCAGATGCC 569
 Db 998 ATGCCAEGGACCTGGTACCTGCCACCATGTCCTGTTCATCAAGGATCCGGTAAACATG 1057
 Qy 1469 AGGCACAAACTAACCCCAAAGATTCGCACTCAGGTGCGGCTCTTGCAAGAAGGCAACGGCCTC 1528
 Db 1253 CTGGCTGGATGGTAACTGAAGCTTGGCCGTTGGATTCTGTGTTACG 1312
 Qy 570 CGGCACAAACTAACAGATGCCCTGGTGGAGTGGCTATGGCAAGCATGGCATT 629
 Db 1058 CTGGGTGACTTGGTGTGGTGGGGTGTGCGAAAACCTGGTGTCTCG 1117
 Qy 1529 GAGTAGCATTAATGTCCTCCGTCGTTGGCCTCTGTCGGGTTGTGAAGGGGCTCAAGGAA 1588
 Db 630 GAATACAGGAGAGCCGCTACTGAGGGCCCTGCTGGACATCATCAGGTCCTGAAGAAG 689
 Qy 1313 TTGAGTCACAATGGAAGGGGTTACAATGAATCG-----AAGGACTTGTG 1360
 Db 1118 CTCAACCACAAACGGTATGCCCTGTGATCTCGAACGGAGGGGTGATATGGATTCTIC 1177
 Qy 1589 ATTG 1592
 Db 690 TCTG 693

RESULT 7
 US-09-227-613-6
 ; Sequence 6, Application US/09227613A
 ; Patent No. 6432684

; GENERAL INFORMATION:
 ; APPLICANT: MUKERJI, Pradip
 ; APPLICANT: LEONARD, Amanda E.
 ; APPLICANT: HUANG, Yung-Sheng
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/227, 613A
 ; CURRENT FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: US/09/227, 610
 ; PRIORITY FILING DATE: 1997-04-11
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 1686
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-09-227-613-6

Query Match 4.7%; Score 96; DB 4; Length 1686;
 Best Local Similarity 59.5%; Pred. No. 1.4e-17;
 Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

Qy 1292 TTGTGGGATTCTGGTTACGTTGAGTGTGTTACATGAAATCGAA- 1350
 Db 390 TGGTTGGTGGGTCAACAGATGAATCGATCGTCAATGGAGATGGCCTAC 449
 Qy 1351 -GGACTCTGTGAGAGCCCAGTTATTACCCCGTAACCAAGGGAGCTGGTTCAAC 1408
 Db 450 CGTGACTGGTTCASTGCCAGCTGACAGCCACCTGCAACTGTCCTCAAC 509
 Qy 1409 GATTGGTTCACTGGGGACTCGAACCCGAGATTGAGCATCACCTGTTCCAACAAATGCC 1468
 Db 510 GACTGGTTCACTGGGACACCTTAACCTCCAGATTGAGCAACCTCCACATGGCATT 569
 Qy 1469 AGGCACAAACTAACCCAAAGATCGCACCTCGAGGCTCTTGGCAAGAAGCGGGCTC 1528
 Db 570 CGGCACAAACTAACAGATGCCCTGGTGGAGTGGCATGGCATT 629
 Qy 1529 GAGTAGCATTAATGTCCTCCGTCGTTGGCCTCTGTCGGGTTGTGAAGGGGCTCAAGGAA 1588
 Db 630 GAATACAGGAGAGCCGCTACTGAGGGCCCTGCTGGACATCATCAGGTCCTGAAGAAG 689

RESULT 8
 US-09-439-261-7
 ; Sequence 7, Application US/09439261
 ; Patent No. 6428990

Qy 1292 TTGTGGGATTCTGGTTACGTTGAGTGTGTTACATGAAATCGAA- 1350
 Db 390 TGGTTGGTGGGTCAACAGATGAATCGATCGTCAATGGAGATGGCCTAC 449
 Qy 1351 --GGACTCTGTGAGAGCCCAGTTATTACCCCGTAACCAAGGGAGCTGGTTCAAC 1408
 Db 450 CGTGACTGGTTCASTGCCAGCTGACAGCCACCTGCAACTGTCCTCAAC 509

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
Mukerji, Pardip
Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng

TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

FILE REFERENCE: 6295-US-P2

CURRENT APPLICATION NUMBER: US/09/439, 261

CURRENT FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: US 08/833, 610

PRIOR FILING DATE: 1997-04-11

PRIOR APPLICATION NUMBER: PCT/US98/07422

PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: US 09/227, 613

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 7

LENGTH: 1843

TYPE: DNA

ORGANISM: Homo sapiens

US-09-439-261-7

Query Match 4.7%; Score 96; DB 4; Length 1843;
Best Local Similarity 59.5%; Pred. No. 1.4e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

Qy 1292 TTGTTGGATTACGTGAGTCAATGGAAAGGTTACAATGAATCGAA- 1350
Db 547 CGTGACTGGTTCACTGGGACCCACCTTAACATGGATGAAATCACATCGTCATGGAGTTGACCAGGGCTTAC 606

Qy 1351 --GGACTTCGTGAGGCCAGGTATTACCAACCGTAACATGGAAAGGTTACAATGAATCGAA- 1350
Db 607 CGTGACTGGTTCACTGGGACCCACCTTAACATGGATGAAATCACATCGTCATGGAGTTGACCAGGGCTTAC 606

Qy 1409 GATTTGGTTCACTGGGGACTCGACACCCAGATTGAGCATCACCTGAAACCTGCAACGTGGAGCAGTCCTTC 1468
Db 667 GACTGGTTCACTGGGACACCTTAACATGGATGAAATCACATCGTCATGGAGTTGACCAGGGCTTAC 726

Qy 1469 AGGCACAAACTACCCCAAGATCGAACCTCAGGTGAGGGCTCTTGCAGAAGGCAGGGCTTC 1528
Db 727 CGGCACAAACTTACACAGATGCCCTGGTGAAGTCTCTATGTGCCLAGGATGGCTATT 786

Qy 1529 GAGTACGGATAATGTTCTCCGTGTTCTGGCTCTGTGCGGGTTGTGAAGGGCTCAAGGAA 1588
Db 787 GAATACCGGAGAAGGCCGCTACTGAAGGGCCCTGCTGGACATCATCAGGTCCCTGCTGAAGAAG 846

Qy 1589 ATTG 1592

Db 847 TCTG 850

RESULT 9
US-09-439-261-8

Sequence 8, Application US/39439261
Patent No. 6428990

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
Mukerji, Pardip
Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng

TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

FILE REFERENCE: 6295-US-P2

CURRENT APPLICATION NUMBER: US/09/439, 261

CURRENT FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: US 08/833, 610

PRIOR FILING DATE: 1997-04-11

PRIOR APPLICATION NUMBER: PCT/US98/07422

PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: US 09/227, 613

PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 60

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 2257

TYPE: DNA

ORGANISM: Homo sapiens

US-09-439-261-8

Query Match 4.7%; Score 96; DB 4; Length 2257;
Best Local Similarity 59.5%; Pred. No. 1.6e-17;
Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;

Qy 1292 TTGTTGGATTACGTGAGTCAATGGAAAGGAGGTACAATGAATCGAA- 1350
Db 961 TGTTTGTGGGTCAACAGATGAAATCACATCGTCATGGAGTTGACCAGGGCTTAC 1020

Qy 1351 --GGACTTCGTGAGGCCAGGTATTACCAACCGTAACATGGAAAGGTTACAATGAATCGAA- 1350
Db 1021 CGTGACTGGTTCACTGGGACTCGACACCCAGCTGAAACCTGCAACGTGGAGCAGTCCTTC 1080

Qy 1409 GATTTGGTTCACTGGGACTCGACACCCAGCTGAAACCTGCAACGTGGAGCAGTCCTTC 1468
Db 1081 GACTGGTTCACTGGGACACCTTAACCTGGACATGAGCACACCTCTCCCCACCATGCCC 1140

Qy 1469 AGGCACRACTACCCCAAGATCCACCTCAAGCTGGGCTCTTTCAGAAGCAGGGCTC 1528
 Db 1141 CGGCACRACTAACAAAGATGCCGCTGGTGAAGCTCATGGCATT 1200

Qy 1529 GAGTAGATAATGTCTCCGTCGTTGGTGCCTCTGTGGCTTAAGGGAA 1588
 Db 1201 GAATACCGGAGAACCGCTACTGAGGGCCTGCTGACATCATCAGTCCCTGAAGAG 1260

Qy 1589 ATTG 1592
 Db 1261 TCTG 1264

RESULT 11
 US-09-227-613-8
 ; Sequence 8, Application US/09227613A

; Patent No. 6432684

; GENERAL INFORMATION:

; APPLICANT: MUKERJI, Pradip

; APPLICANT: LEONARD, Amanda E.

; APPLICANT: HUANG, Yung-Sheng

; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

; FILE REFERENCE: 6295.US.P1

; CURRENT APPLICATION NUMBER: US/09/227,613A

; CURRENT FILING DATE: 1999-01-08

; PRIOR APPLICATION NUMBER: 08/833,610

; PRIOR FILING DATE: 1997-04-11

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 2257

; TYPE: DNA

; ORGANISM: Homo Sapien

; US-09-227-613-8

Query Match 4.7%; Score 96; DB 4; Length: 2257;
 Best Local Similarity 59.5%; Pred. No. 1.6e-17;
 Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
 US-09-227-613-8

Qy 1292 TTGTTGGATTCTGTGTTACGGTCAACATGGAAAGGGACGTTTACAATGAAATCGAA- 1350
 Db 961 TGTTTGTGGGTACACAGATGAATCACATCGTCATGGAGATTGACCGAGGGCTAC 1020
 Qy 1351 -GGACTTCGTGAGGCCAGGTATTACCAACCCGTAAACAGCGAGGCTGGTCAAC 1408
 Db 1021 CGTGACTGGTTCAAGTAGCCACCTGACAGCCACCTGAAACGTGGAGCTCCCTCAAC 1080

Qy 1409 GATTGGTTCACTGGGGACTCGACACCCAGATTGAGCATCACCTGTTCCAACAATGCC 1468
 Db 1081 GACTGGTTCACTGGACACCTTAACCTCCAGATTGACCCACCTCTCCCACCATGCC 1140

Qy 1469 AGGCACRACTACCCAAAGATCGCACCTCAGGTGAGGCTCTTGCAGAACGGCTC 1528
 Db 1141 CGGCACRACTAACAAAGATGCCCGCTGGTGAAGCTCATATGTGCCAAGCATGGCAT 1200

Qy 1529 GAGTAGATAATGTCTCCGTCGTTGGCCCTCTGTGGCTGTGAAGGGCTCAGGAA 1588
 Db 1201 GAATACCGGAGAACCGCTACTGAGGGCCCTGCTGACATCATCAGTCCCTGAAGAG 1260

Qy 1589 ATTG 1592
 Db 1261 TCTG 1264

RESULT 12

US-09-023-655-295

; Sequence 295, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

Qy 1589 ATTG 1592
 Db 1261 TCTG 833

RESULT 13
 US-09-769-863-13
 ; Sequence 13, Application US/09769863
 ; Patent No. 6635451

Qy 1589 ATTG 1592
 Db 1261 TCTG 833

COMPUTER READABLE FORM:
 COMPUTER MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023,655
 FILING DATE: 09/023,655
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Zeller, Karen J.
 REGISTRATION NUMBER: 37,071
 REFERENCE/DOCKET NUMBER: PA-0001 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 855-0555
 TELEFAX: (650) 845-4166
 INFORMATION FOR SEQ ID NO: 295:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2540 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: PROSNOT11
 CLONE: 1346478

Query Match 4.7%; Score 96; DB 4; Length: 2540;
 Best Local Similarity 59.5%; Pred. No. 1.7e-17;
 Matches 181; Conservative 0; Mismatches 120; Indels 3; Gaps 1;
 US-09-023-655-295

Qy 1292 TTGTTGGATTCTGTGAGAGGCCAGGTATTACCAACCCGTAAACAGCGAGGCTGGTCAAC 1408
 Db 530 TGGTTTGTGGGTCAACACAGATGAATCATCGTCATGGAGATTGACCCAGGGCTAC 589

Qy 1351 -GGACTTCGTGAGGCCAGGTATTACCAACCCGTAAACAGCGAGGCTGGTCAAC 1408
 Db 590 CGTGAATGGTTCACTGAGCCAGGTGACAGCCACCTGCAACGTGGAGCTTCCTCAAC 649

Qy 1409 GATTGGTTCACTGGGGACTCGACACCCAGATTGAGCATCACCTGTTCCAACAATGCC 1468
 Db 650 GACTGGTTCACTGGACACCTTAACCTCCAGATTGACCCACCTTCCCACCATGCC 709

Qy 1469 AGGCACRACTACCCAAAGATCGCACCTCAGGTGAGGCTCTTGCAGAACGGCTC 1528
 Db 710 CGGCACAACTACCCCAAGATCGCACCTCAGGTGAGGCTCTTGCAGAACGGCTC 1528

Qy 1529 GAGTAGATAATGTCTCCGTCGTTGGCCCTCTGTGGCTGTGAAGGTCTCATATGTGCCAAGGAA 1588
 Db 773 GAATACCGGAGAACCGCTACTGAGGGCCCTGCTGACATCATCAGTCCCTGAAGAAG 829

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
Mukerji, Pradip
APPLICANT: Fuang, Yung-Sheng
APPLICANT: Das, Tapas
APPLICANT: Thurmond, Jennifer
APPLICANT: Pereira, Suzette L.

TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF

FILE REFERENCE: 6763-US-01

CURRENT APPLICATION NUMBER: US/09/769, 863

CURRENT FILING DATE: 2001-01-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 13

LENGTH: 1362

TYPE: DNA

ORGANISM: Saprolegnia diclina

US-09-769-863-13

Query Match 4 - 4%; Score 90.2; DB 4; Length 1362;
Best Local Similarity 47.4%; Pred. No. 5.8e-16;
Matches 429; Conservative 0; Mismatches 443; Indels 33; Gaps 4;

QY 756 TGCTGTCAAGCCAGTTGATGGGTCTTCTGTCCACAGTGTGGATGGCTGCCATGATT 815
DB 458 TGGTCGGGCTGTCATCCTGGCCCTTTACCGCAGTGGGGCTGGCTGCCATGACT 517

QY 816 TCCTTCATCAAACGGCTCTTGAGAACCGTACCCGCGPACTCCTCTTTGGCTATTGGTCG 875
DB 518 TTCTGCACCCACCAAGCTGGAAACCACCTGGTGGAAACCATGGTGGCTCATGGTCG 577

QY 876 GCAATTGGTGGCTTACTGTATCATGGTGGAAAGCACAAACATTCACTATA 935
DB 578 GCAACCTCTGGCAGGGCTCTCGGTGGAGAACACAGCAACACGGCACCARG 637

QY 936 CTGCTCCGA-----ATGAGTCGACGAAAGTAGTACACCTCTAGACGAAGACATTGATA 989
DB 638 CGATCCCACACTCACCGGACGCCAGATGCCCTCCACGGGACATGGACA 697

QY 990 CTCTCCCCATCATGGCTGCTGGCAAGGGCTCTCGGTGGAGAACACAGCAAGAGAA 1046
DB 698 CGATGCCGATTCTCGGTGGCTCAAGATGGCGAGCACGCGACTGCCGTG 757

QY 1047 TTTTGGGAGTGCTCAATACTGGCACTACATGATTGCTCTTGTTCATGGCCGGT 1106
DB 758 GGCTCTCTTCATGGCTACCAAGCTGACTTCCATCTCTGCTCTTGGCGGTA 817

QY 1107 ACAGTTGGACTTTGGAAAGTTGGCTCTCACATTCACTCTGATTGAGCAGGACCA--- 1163
DB 818 TCTCGTGGGTGATCCAGTCGGCCATAGTACGCCCTTACAACGTTGGCCGGGACCT 877

QY 1164 -----AGGGATTGATAGAGAAGGGAAACAGTTGCTTTCACTACGCTCTGGT 1208
DB 878 TTGACAAGGGTCCAGTACCCGGCTGCTCGGGCCGCGGCTCTACTACGCTGGGA 937

QY 1209 TCAGTTGGGCTGGTCCATATTTCGGGGTTGGGATTGCTGGCTTAAGCCTTGTGGTAG 1268
DB 938 ACCTCGGCTTGTGTGACGGAGCAACATGTGCTGCTGCTGGCTGGCTCTCTTC 997

QY 1269 CAACTGAGCTTGTGGCCGGCTTACGGGATTGCTGGTTACGGTGAAGTCACAATGGAA 1328
DB 998 TGAGCCAGGGCTGCTGGGGCTCTTCCCTGGCATGGTGGCCACAAAGGGC 1057

QY 1329 AGGAGGTT----ACAATGAAATCGAAGGACTTCGAGGCTGAGGCCCAAGCC 1382
DB 1058 TGGAGGTCTTGTGACAGGACAGCAAGCCGGATTTGGAAAGTGTCAAGTGTGACAC 1117

QY 1383 GAAACACAAAGGAGGGCTGGTTAACGATGGTTCAACTGGCTGAACTGGGGATG 1442
DB 1118 GCAAAGTGAAGTGTGCTGGCTCTGAACTGGGTCAAGTGGCTCAACTACAGATG 1177

QY 1443 AGCATCACCTGTTCCAACAAATSSCCAAAGGACAAACTACCCCAAGATGCACTCAGSTCG 1502

Query Match 4 - 3%; Score 87.6; DB 4; Length 1717;
Best Local Similarity 59.8%; Pred. No. 3.8e-15;
Matches 147; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1351 GGACTTCGTTGAGAGCCAGGGTATACCAAGCCAGTAACCAAGCCAGTGGCTAACGA 1410
DB 1136 GAATGGGTAGCTGGCCACCTGCAACTTTCAGCTGGAGGCCCTCACTTTACCAA 1195

QY 1411 TGGTTCACTGGGGACTCGACACCCAGATTGAGCATCACCTGTTCCAACAAATGCCAG 1470

Db 1196 CTGGTTCAGGGCACCTCAACTTCCAGATCGAGGCCACCTTTCCCAGGGATGCGAG 1255
 QY 1471 GCACAACCTACCCAAAGATCGAACCTCAGGTGAGGCCTTTGCAAAGAACACTCAATGACTACTAC 562
 Db 1256 ACACAACCTACAGCGGCTGCCGCTGCAAGTCGCTGTCAGCCAAGCAGGGCTCAG 1530
 QY 1531 GTACGATAATGTCCTCCGTCGTTGGTGCCTCTGTGCGGTTGTGAAGGGCTCAAGGAATT 1590
 Db 1316 CTACGAAGTGAAGGCCCTCCACGGCCTGGACATCGTAGGTCCCTGAAGAAGTC 1375
 QY 1591 TGCTGA 1596
 Db 1376 TGCTGA 1381
 Db RESULT 15
 US-08-831-570-1
 Sequence 1, Application US/08831570
 Patent No. 5959175
 GENERAL INFORMATION:
 APPLICANT: Thomas, Terry L.
 APPLICANT: Nurberg, Andrew N.
 APPLICANT: Beremand, Phillip D.
 TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
 TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
 TITLE OF INVENTION: COMPOSITION
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: USA
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/831,570
 FILING DATE: 09-APR-1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: DIGILIO, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 10545
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 743-4366
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1684 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 43..1387
 US-08-831-570-1

QY 503 ACAGACGTTTCGCAACATCCACCTGGCATCGGAAGCAACTCAATGACTACTAC 562
 Db 211 ACTCTGCAATTGGTGCATTCCATCTGCCTCTACATGGAAATCTGATAAGTTTTC 270
 QY 563 ATTGGAGACCCCTGCTAGGGAAAGGCCCTGATGATTTGCTTAAGGACTACAGAGATATG 622
 Db 271 ACTGGGTATTATCTAAAGATTACTCTGTTCTGAGGTCTAAAGATTATAGGAAGCTT 330
 QY 623 AGAGCCGGTTGGTAAAGAGGCTTTCAAGAGTTCAAGSCTGGTTCTCGCTTCAG 682
 Db 331 GTGTTTGAGTTTCTAAATGGTTGTATGACAAAAAGGTCAATTATGTTGCAACT 390
 QY 683 ACTCTGATAATGCAGCTCTTGTGCTGAGGACTATCTGTTACGACAAGAGT 742
 Db 391 TTGTCCTTATGCAATTGCTGTTGCTATGAGTGTGTTATGGGTTATGGTTGAGGTT 450
 QY 743 TACTGGCTATTGCGCTGCTGAGCTCTTGTGCTGAGGCTCTTGTGTTGAGGTT 802
 Db 451 GTTTRGGTACATTGTTCTGGATTCAAGGTTCTTGGTTGATGGGTTCTGGTTGAGGTTGG 510
 QY 803 CTGCCCCATGATTCCCTCATCACAGGTCTTGGAACTCCCTCTT 862
 Db 511 ATTGGACATGATGCTGGCATTATGGTAGTGTCTGATTCAAGGTTCTGGTTGAGGTTGG 570
 QY 863 GGCTATTGTTGGCAATTGCGTGCCTTAGTGTATCATGGTGGCTT 922
 Db 571 GGTATTGCTGCAATTGCTTCAAGGATAAGTATGGTTGGAAATGGAAACCAT 630
 QY 923 AACATTCACTCATACTGCTCCGAAT 946
 Db 631 ATGCAACATCACATTGCTGTAAT 654

Search completed: June 19, 2004, 02:39:11
 Job time : 164 secs

Query Match 4..3%; Score 87.2; DB 2; Length 1684;
 Best Local Similarity 48.4%; Pred. No. 4..9e-15;
 Matches 273; Conservative 0; Mismatches 288; Indels 3; Gaps 27

QY 386 CACGACAGGCCTGGAGACTGCTGGATGATCGTCAAAGAGAAAGGTGTATGATATTAGCCGT 445
 Db 91 CACGATAAACCCGGAGATCTAGGATCTCGATTCAAGGAAAGCCTATGATGTTTCGAAAT 150
 QY 446 TTTGGGAGGACCAACCCCTGGAGGGACGGT---AATTAGCCCTACTTTGGGGGGAT33C 502
 Db 151 TGGTGAAGACCATCCAGGTGGCAAGGTCTTCCCTGAAGAGTCTTGGCTTCAAGAGGTA 210

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:03:22 ; Search time 59 Seconds
(without alignments)
2313.058 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDLFNLFTWSKYSV.....AVVKALKEIADEASIRLHAAH 483

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04;*
1: geneseqp1980s;*
2: geneseqp1990s;*
3: geneseqp2000s;*
4: geneseqp2001s;*
5: geneseqp2002s;*
6: geneseqp2003as;*
7: geneseqp2003bs;*
8: geneseqp2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	2595	100.0	483	4 AAB46436	Aab46436 C. purpur
2	2595	100.0	483	4 AAB46435	Aab46435 C. purpur
3	1619	62.4	520	4 AAB46440	Aab46440 C. purpur
4	1475	56.8	525	3 AAY51354	Aay51354 Protein b
5	1475	56.8	525	4 AAB46810	Aab46810 P. patens
6	1475	56.8	525	5 ABB98277	Abb98277 Physcomit
7	1475	56.8	525	5 ABG73602	Abg73602 P. patens
8	1475	56.8	525	5 ABG73607	Abg73607 P. patens
9	1475	56.8	525	5 ABG94707	Abg94707 Human del
10	929	35.8	173	4 AAB46437	Aab46437 C. purpur
11	841.5	32.4	457	2 AAW84137	Aaw84137 A delta-6
12	841.5	32.4	457	2 AAW95504	Aaw95504 Mortierell
13	841.5	32.4	457	3 AAY56045	Aay56045 Fungal de
14	841.5	32.4	457	3 AAY92599	Aay92599 M. alpina
15	841.5	32.4	457	4 AAB31684	Aab31684 Amino aci
16	841.5	32.4	458	5 ABG96527	Abg96527 M. alpina
17	841.5	32.4	458	5 ABG96509	Abg96509 M. alpina
18	841.5	32.4	458	5 ABG94707	Abg94707 Human del
19	841.5	32.4	458	5 ABG94693	Abg94693 A delta-6
20	839.5	32.4	457	2 AAW85121	Aaw85121 Phaeodact
21	799.5	30.8	477	5 ABB98275	Abb98275 P. tricorn
22	799.5	30.8	477	5 ABG73600	Abg73600 Saprolegn
23	798.5	30.8	453	6 AAE31900	Aae31900 Pythium i
24	790	30.4	459	5 AAE22063	Aae22063 Amino aci
25	705.5	27.2	467	6 ABB99479	Abb99479 Amino aci

RESULT 1
AAB46436
ID AAB46436 Standard; protein; 483 AA.
XX
AC AAB46436;
XX
DT 06-APR-2001 (First entry)
XX
C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 4.
XX
DE
XX
KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid; transgenic plant; plant oil; triglyceride; nutrition; animal feed; cosmetic.
XX
OS Ceratodon purpureus.
XX
PN WO200075341-A1.
XX
PD 14-DEC-2000.
XX
PP 07-JUN-2000; 2000WO-EP005274.
XX
PR 07-JUN-1999; 99DE-01025718.
PR 22-DEC-1999; 99DE-01062409.
XX
PA (BADI) BASF AG.
XX
PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;
XX
WPI; 2001-112150/12.
DR N-PSDB; AAF25730.
XX
PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.
XX
PS Example 8; Page 49-50; 69pp; German.

This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (II), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (IIa); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other

CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and to isolate related sequences by
 CC homology screening. (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (II), resulting in oils with increased
 CC content of saturated fatty acids

XX SQ Sequence 483 AA;

Query Match Score 2595; DB 4; Length 483;
 Best Local Similarity 100.0%; Prid. No. 3.8e-266;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALVTDFLNFLGTTWSKSYVTTESYAGNYGPTLKHAKKVSAOGKTAGGTLRQRSVQDKKP 60
 Db 1 MALVTDFLNFLGTTWSKSYVTTESYAGNYGPTLKHAKKVSAOGKTAGGTLRQRSVQDKKP 60

Qy 62 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120
 Db 61 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120

Qy 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180
 Db 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180

Qy 181 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240
 Db 181 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240

Qy 241 SVSWWRTRKHNIHHTAPNECDQQYTPLDEDIDTLPIIAWSKEILLATESKRILRVLYQHY 300
 Db 241 SVSWWRTRKHNIHHTAPNECDQQYTPLDEDIDTLPIIAWSKEILLATESKRILRVLYQHY 300

Qy 301 MILPLLPMARYSTFGSLLFTENPDLSITKGLIEKGTVAFHYAWPSWAAFHILPGVAKPL 360
 Db 301 MILPLLPMARYSTFGSLLFTENPDLSITKGLIEKGTVAFHYAWPSWAAFHILPGVAKPL 360

Qy 361 AWWVATELVAGLLLGFPVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGWFNDWFTGGLCT 420
 Db 361 AWWVATELVAGLLLGFPVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGWFNDWFTGGLCT 420

Qy 421 QIEHHLEPTMPRHNPYKPIAPQVEALCKKHLGLBYDNVSVVGASVAVVKALKEIADEASIRL 480
 Db 421 QIEHHLEPTMPRHNPYKPIAPQVEALCKKHLGLBYDNVSVVGASVAVVKALKEIADEASIRL 480

Qy 481 HAH 483
 Db 481 HAH 483

RESULT 2
 ID AAB46435 standard; protein; 483 AA.
 AC AAB46435;
 XX DT 06-APR-2001 (first entry);
 DE C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 2.
 XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic.
 XX OS Ceratodon purpureus.
 XX PN WO2000075341-A1.
 XX PD 14-DEC-2000.
 XX PF 07-JUN-2000; 2033WO-EPO05274.
 XX

PR 07-JUN-1999; 99DE-01025718.	
PR 22-DEC-1999; 99DE-01062409.	
XX (BADI) BASF AG.	
PA	
XX Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;	
XX DR WPI; 2001-112150/12.	
DR N-PSDB; AAF25729.	
XX PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.	
XX PS Example 8; Page 44-46; 69pp; German.	
XX This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I); (e) preparation of (c); (f) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (g) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids	
XX SQ Sequence 483 AA;	
Query Match Score 2595; DB 4; Length 483;	
Best Local Similarity 100.0%; Prid. No. 3.8e-266;	
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Query Match Score 2595; DB 4; Length 483;	
Best Local Similarity 100.0%; Prid. No. 3.8e-266;	
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY 1 MALVTDFLNFLGTTWSKSYVTTESYAGNYGPTLKHAKKVSAOGKTAGGTLRQRSVQDKKP 60 Db 1 MALVTDFLNFLGTTWSKSYVTTESYAGNYGPTLKHAKKVSAOGKTAGGTLRQRSVQDKKP 60	1 MALVTDFLNFLGTTWSKSYVTTESYAGNYGPTLKHAKKVSAOGKTAGGTLRQRSVQDKKP 60 1 MALVTDFLNFLGTTWSKSYVTTESYAGNYGPTLKHAKKVSAOGKTAGGTLRQRSVQDKKP 60
Qy 62 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120 Db 61 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120	61 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120 61 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120
Qy 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180 Db 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180	121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180
Qy 181 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240 Db 181 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240	QY 1 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240 Db 1 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240
Qy 241 SVSWWRTRKHNIHHTAPNECDQQYTPLDEDIDTLPIIAWSKEILLATESKRILRVLYQHY 300 Db 241 SVSWWRTRKHNIHHTAPNECDQQYTPLDEDIDTLPIIAWSKEILLATESKRILRVLYQHY 300	QY 61 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120 Db 61 GTYSLADVASHDRPGDCWMIVKVKYDIDSRFADDHPGGTVISTYFGRDGTDVFATFHPPA 120
Qy 301 MILPLLPMARYSTFGSLLFTENPDLSITKGLIEKGTVAFHYAWPSWAAFHILPGVAKPL 360 Db 301 MILPLLPMARYSTFGSLLFTENPDLSITKGLIEKGTVAFHYAWPSWAAFHILPGVAKPL 360	QY 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180 Db 121 AWKQLNDYYIGDLAREEPLDELLKDYRDRAEFVREGFLFKSSKAWFLQTLINAALFAAS 180
Qy 361 AWWVATELVAGLLLGFPVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGWFNDWFTGGLCT 420 Db 361 AWWVATELVAGLLLGFPVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGWFNDWFTGGLCT 420	QY 181 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240 Db 181 IATICYDKSYWAIILSASLMGLFVQQCGWLAHDFLHQOQFENRTANSFFGYLFGNCVLFGF 240
Qy 421 QIEHHLEPTMPRHNPYKPIAPQVEALCKKHLGLBYDNVSVVGASVAVVKALKEIADEASIRL 480 Db 421 QIEHHLEPTMPRHNPYKPIAPQVEALCKKHLGLBYDNVSVVGASVAVVKALKEIADEASIRL 480	QY 241 SVSWWRTRKHNIHHTAPNECDQQYTPLDEDIDTLPIIAWSKEILLATESKRILRVLYQHY 300 Db 241 SVSWWRTRKHNIHHTAPNECDQQYTPLDEDIDTLPIIAWSKEILLATESKRILRVLYQHY 300
Qy 481 HAH 483 Db 481 HAH 483	QY 301 MILPLLPMARYSTFGSLLFTENPDLSITKGLIEKGTVAFHYAWPSWAAFHILPGVAKPL 360 Db 301 MILPLLPMARYSTFGSLLFTENPDLSITKGLIEKGTVAFHYAWPSWAAFHILPGVAKPL 360
XX	QY 361 AWVATELVAGLLLGFPVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGWFNDWFTGGLCT 420 Db 361 AWVATELVAGLLLGFPVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGWFNDWFTGGLCT 420
XX	QY 421 QIEHHLEPTMPRHNPYKPIAPQVEALCKKHLGLBYDNVSVVGASVAVVKALKEIADEASIRL 480 Db 421 QIEHHLEPTMPRHNPYKPIAPQVEALCKKHLGLBYDNVSVVGASVAVVKALKEIADEASIRL 480
XX	QY 481 HAH 483

CC -8-unsaturated long-chain base cis/trans ratio, especially to compensate
 CC for a delta-8-unsaturated long-chain base deficiency, to exclude
 CC production of delta-8-unsaturated bases, to increase tolerance or
 CC resistance to soil salinity, ion stress or toxicity, drought, wet
 CC conditions, cold or frost and/or phytopathogenic microorganisms, or to
 alter size growth and flowering time. Cells, transgenic organisms or
 plants containing the DNA sequence can be used to produce sphingolipids
 and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
 can be used in cosmetics, pharmaceuticals and foods and as chemical raw
 materials. This sequence represents a protein which has delta₆ fatty acid
 desaturase activity which is described in the method of the invention

XX SQ Sequence 525 AA;
 Query Match 56.8%; Score 1475; DB 3; Length 525;
 Best Local Similarity 55.3%; Pred. No. 4e-147;
 Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

```

  1  MALVTDLFNLFDT---WSKYSVYTHSYA-SNYGPTLKHAKKVS----- 40
  25  MSLFSDPESYVSSTVGWSVHSIQLPK----RLTSKRVSEAAVQCISAEVQRNSS 77
  41  -----AQKTAGQTLRQRSVQDKKPGTYSLADVAASHDRPGDCWMIVKERYTDISRFADD 94
  78  TOGTAEALAESVVKPTRLSSQWKK-STHPSEAVAHNKPSDCWIVVZKRYDVSNADE 136
  QY  95  HPGGTIVSITYFGRDGTDVATFPAAWKQLNDYYIGDLAREEPDELKDYRDMRAEFFV 154
  137  HPGGSVISTYFGRDGTDVFSSEHAATSWKILQDFYIGDVERVEF-PELLKDREMRAFL 196
  QY  155  REGLFKSKAWELLCTLLNAALFAASIAITCYDKSYWAIWLSASIMGLFVQOCGWLIAHDF 214
  Db  197  REQLFKSKLYYYYMKLTTNVAFFAASTAIICWSKTTISAVLASACMMALCFQQCGWLSHDF 256
  QY  215  LHQQVQEENRTANSFEGTYLFGNCVLGFSVSWWRTRKHNIIHTAPNECDEQYTPLDEDIDTL 274
  Db  257  LHNQVFETRWLNENVGYVIGNAYVLGFSTGWWKEKHNLHAAAPNECDQTYQPIDEDIDTL 316
  QY  275  LIAWSKELIATVESKRILRVLQYQHMYMLPPLFMPM-RYWTGSSLFTNPDLSTTKGLIE 334
  Db  317  LIAWSKDIILATVENKTFLRILQYQHLMFFGMLLFFARGSWLFWSWRYTSTAFLSPVDRJLE 376
  QY  335  KGTVAZHYAWFSAWAHFHILPGVAKPLAWMATELVAGLILLGFVETLSSHNGKEVYNESKDF 394
  Db  377  KGTVLFHYYFWFVGTACYLPG-WKPLVWWAVTELMSGMLLGFVETLSSHNGMEVYNSSKEF 435
  QY  395  VRAQVITTRNTKRGWENDWETGGLDTQIEHHLPPTMPRNYPKLAPOVEALCKKHGLEYD 454
  Db  436  VSQIIVSTRODIKGNIENDWETGGLNQIEHHLPPTMPRNINKAPRVEVFCKKHGLMYE 495
  QY  455  NVSVVGASVAVVKALKELIADEASISTRHLA 482
  Db  496  DVSIATGTCVKLKALKEVA-EEAAEQHA 522
  
```

RESULT 5
 AAB46810 standard; protein: 525 AA.
 ID AAB46810
 AC AAB46810;
 DT 23-APR-2001 (first entry)
 DE P. patens delta₆-desaturase protein.
 XX Delta₆-desaturase; unsaturated fatty acid; transgenic; oil; lipid;
 KW fatty acid; human nutrition; animal nutrition; cosmetic; pharmaceutical;
 KW agricultural chemical.
 XX OS Physcomitrella Patens.
 XX WO200102591-A1.
 EN 335 KGTVAZHYAWFSAWAHFHILPGVAKPLAWMATELVAGLILLGFVETLSSHNGKEVYNESKDF 394
 377 KGTVLFHYYFWFVGTACYLPG-WKPLVWWAVTELMSGMLLGFVETLSSHNGMEVYNSSKEF 435
 XX 395 VRAQVITTRNTKRGWENDWETGGLDTQIEHHLPPTMPRNYPKLAPOVEALCKKHGLEYD 454

CC	PD	11-JAN-2001.
CC	XX	
CC	PF	04-JUL-2000; 2000WO-EP006223.
CC	XX	
CC	PR	06-JUL-1999; 99US-00347531.
CC	PR	30-JUN-2000; 2000DE-01030976.
CC	XX	
CC	PA	BADI) BASF AG.
CC	XX	
CC	PI	Heinz E, Girke T, Scheffler J, Da Costa E SilvaO;
CC	XX	
CC	WPI;	2001-123117/13.
CC	DR	N-PSDB; AAF26040.
XX	XX	
PT	Production of unsaturated fatty acids, useful e.g. in nutrition,	
PT	cosmetics or pharmaceuticals, in organisms transformed with	
PT	Physcomitrella patens delta-6-desaturase nucleic acid.	
XX	BS	Claim 1c; Page 41-43; 49pp; German.
XX	CC	This invention describes a novel preparation of unsaturated fatty acids (II) by introducing into an organism at least one isolated nucleic acid (II) that encodes a polypeptide (III), with Delta ₆ -desaturase activity. Organisms that contain at least 1 wt.-% (II), on total fatty acid content, are then selected. (II) is selected from: (a) a 2012 bp sequence (S1), defined in the specification, or its equivalents within the degeneracy of the genetic code; or (b) derivatives of the sequence of (a) that encode a 525 amino acid polypeptide (S2), defined in the specification, or a polypeptide with at least 50% homology with (S2) and practically the same enzymatic activity. The invention also describes (1) transgenic organisms that contain (II); and (2) oils, lipids and fatty acids produced by the new method. The oils, lipids and fatty acids produced by the transformed organisms are used in human or animal nutrition, cosmetics, pharmaceuticals and agricultural chemicals. (III) can also be used, in vitro, for increasing the (II) content of triglycerides. The transgenic organisms have increased contents of (I), or of (II)-containing triglycerides, particularly of gamma-linolenic acid
XX	Sequence 525 AA;	Sequence 525 AA;
Query	Query Match 56.8%; Score 1475; DB 4; Length 525;	
Query	Best Local Similarity 55.3%; Pred. No. 4e-147;	
Matches	Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;	
Db	Matches 281; Conservatve 74; Mismatches 117; Indels 36; Gaps 6;	
QY	1 MALVTDLFNLFDT---WSKYSVYTHSYA-SNYGPTLKHAKKVS----- 40	
Db	25 MSLFSDPESYVSSTVGWSVHSIQLPK----RLTSKRVSEAAVQCISAEVQRNSS 77	
QY	41 -----AQKTAGQTLRQRSVQDKKPGTYSLADVAASHDRPGDCWMIVKERYTDISRFADD 94	
Db	78 TOGTAEALAESVVKPTRLSSQWKK-STHPSEAVAHNKPSDCWIVVZKRYDVSNADE 136	
QY	95 HPGGTIVSITYFGRDGTDVATFPAAWKQLNDYYIGDLAREEPDELKDYRDMRAEFFV 154	
Db	137 HPGGSVISTYFGRDGTDVFSSEHAATSWKILQDFYIGDVERVEF-PELLKDREMRAFL 196	
QY	155 REGLFKSKAWELLCTLLNAALFAASIAITCYDKSYWAIWLSASIMGLFVQOCGWLIAHDF 214	
Db	197 REQLFKSKLYYYYMKLTTNVAFFAASTAIICWSKTTISAVLASACMMALCFQQCGWLSHDF 256	
QY	215 LHQQVQEENRTANSFEGTYLFGNCVLGFSVSWWRTRKHNIIHTAPNECDEQYTPLDEDIDTL 274	
Db	257 LHNQVFETRWLNENVGYVIGNAYVLGFSTGWWKEKHNLHAAAPNECDQTYQPIDEDIDTL 316	
QY	275 LIAWSKELIATVESKRILRVLQYQHMYMLPPLFMPM-RYWTGSSLFTNPDLSTTKGLIE 334	
Db	317 LIAWSKDIILATVENKTFLRILQYQHLMFFGMLLFFARGSWLFWSWRYTSTAFLSPVDRJLE 376	
QY	335 KGTVAZHYAWFSAWAHFHILPGVAKPLAWMATELVAGLILLGFVETLSSHNGKEVYNESKDF 394	
Db	377 KGTVLFHYYFWFVGTACYLPG-WKPLVWWAVTELMSGMLLGFVETLSSHNGMEVYNSSKEF 435	
QY	395 VRAQVITTRNTKRGWENDWETGGLDTQIEHHLPPTMPRNYPKLAPOVEALCKKHGLEYD 454	
Db	436 VSQIIVSTRODIKGNIENDWETGGLNQIEHHLPPTMPRNINKAPRVEVFCKKHGLMYE 495	
QY	455 NVSVVGASVAVVKALKELIADEASISTRHLA 482	
Db	496 DVSIATGTCVKLKALKEVA-EEAAEQHA 522	
QY	56.8%; Score 1475; DB 4; Length 525;	
QY	Best Local Similarity 55.3%; Pred. No. 4e-147;	
Matches	Matches 281; Conservatve 74; Mismatches 117; Indels 36; Gaps 6;	
Db	Matches 281; Conservatve 74; Mismatches 117; Indels 36; Gaps 6;	
QY	1 MALVTDLFNLFDT---WSKYSVYTHSYA-SNYGPTLKHAKKVS----- 40	
Db	25 MSLFSDPESYVSSTVGWSVHSIQLPK----RLTSKRVSEAAVQCISAEVQRNSS 77	
QY	41 -----AOGKTAGOTLQRORSVODKKPGTYSLADVAASHDRPGDCWMIVKERYTDISRFADD 94	
Db	78 TOGTAEALAESVVKPTRLSSQWKK-STHPSEAVAHNKPSDCWIVVZKRYDVSNADE 136	
QY	95 HPGGTIVSITYFGRDGTDVATFPAAWKQLNDYYIGDLAREEPDELKDYRDMRAEFFV 154	
Db	137 HPGGSVISTYFGRDGTDVFSSEHAATSWKILQDFYIGDVERVEFPELKLKDREMRAFL 196	
QY	155 REGLFKSSRAWFLLQTLLNAALFAASIAITCYDKSYWAIWLSASIMGLFVQOCGWLIAHDF 214	
Db	197 REQLFKSSKLYYYMQLLTNVAIIFASASIRIICWSKTIASVLASACMMALCFQQCGWLSHDF 256	
QY	215 LIHQVQFENTRANTSFFGYLFGNCVLTGFSVSWWRTRKHNIIHTAPNECDEQYTPLDEDIDTL 274	
Db	257 LIHNQVFETRWLNENVGYVIGNAVLGFSTGWWKEKHNLHAAAPNECDQTYQPIDEDIDTL 316	
QY	275 LIAWSKELIATVESKRILRVLQYQHMYMLPPLFMPM-RYWTGSSLFTNPDLSTTKGLIE 334	
Db	317 LIAWSKDIILATVENKTFLRILQYQHLMFFGMLLFFARGSWLFWSWRYTSTAFLSPVDRJLE 376	
QY	335 KGTVAZHYAWFSAWAHFHILPGVAKPLAWMATELVAGLILLGFVETLSSHNGKEVYNESKDF 394	
Db	377 KGTVLFHYYFWFVGTACYLPG-WKPLVWWAVTELMSGMLLGFVETLSSHNGMEVYNSSKEF 435	

RESULT 9		QY 1 MAlVTDLNFLLT---WSKYSVYTHSYAGNYGPTIKHAKKYS-----40	
b	377 KGTIVLEHYFWFVGTACYLLPG-WKPLWMMAVTELMSGMLLGFFVLSHNGMEVNNSSKEF	435	DB 25 MSLFSDFFSYVSSTVGSWSVHSIQPLK-----RITSKRVSESAAVQCISAEVQRNS 77
	395 VRAQVITERNTRKGWFDNDWFTGGLDTQIEHLFPTMPRHNPYKIAPOVEAECRKXHGLEYD	454	Db 41 -----AQGKTAGQTILRORSVQDKKPGTYSLADVASHDRPGDCWMIVKEKVYDISRFADD 94
b	436 VSAQIVSTRDIKGNIFNDWFTGGLNRCIIEHLFPTMPRHNLNKTAAPRVEWCKRKXHGVYE	495	Db 78 TQGTABAESVVKPTRLRRSSQWKK-STHPLSEVAHNKPDSDCWIVVWNKYYDVSNFADE 136
	455 NVSVVGASVAVVKALKEIADEASIRLHA 482		QY 95 EPGGTIVLSTYFGRDGTDFATFHPPAAWKOLNDYYIGDLAREEPLDELLKDYRDMAEFV 154
b	496 DVSIATGTCVKVLKALKEVA-EAAAEQHA 522		Db 137 HPGGSVISTYFGRDGTDFATFHPPAAWKOLNDYYIGDLAREEPLDELLKDYRDMAEFV 196
			QY 155 REGLFKSSKAWFLLQTLINNEALFAASIACTCYDKSYWAIILSASIMMGLFVQQCGWLAHDF 214
b			Db 197 REQLFKSSKLYYVMKLLTNVAIFAAASIAICWSKTIASAVLASACMMALCEQQCGWLSHDF 256
			QY 215 LHQQVFBNRTANSFFGYLFGNCVLGFSVSHWRTKNITHHTAPNECDEQYTPLDEDIDTLP 274
b			Db 257 LHNQVFETRWLNEVVGYVIGNAVLGFSTGAWKEKHNLLHAAAPNECDQTYQPIDEIDTLP 316
			QY 275 IIAWSKEILLATESKRILRVLQYQHMYMILLPLFLMARYSWTFGSLLFTENPDLSSTTKGLIE 334
b			Db 317 IIAWSKEILLATEVNKTFLRILQYQHMFARGSWLFWSWRYTSTAVLSPVDRLLIE 376
			QY 335 KGTVAFHAYAFSWAAFHILLPGVAKPLAMMVATELVAGLLLGFTLSHNGKEVYNESKDF 394
b			Db 377 KGTIVLFFHYWFVGTACYLLPG-WKPLWMMAVTELMSGMLLGFFVFLSHNGMEVYNSSKEF 435
			QY 395 VRAQVITTRNTKRGWENDWFTGGLDTQIEHHHLFPPTMPRHNYPKIAQVEALCKRKHGLEYD 454
b			Db 436 VSAQIVSTRDIKGNIFNDWFTGGLNRCIIEHHHLFPPTMPRHNLYLNGMEVYNSSKEF 495
			QY 455 NVSVVGASVAVVKALKEIADEASIRLHA 482
b			Db 496 DVSIATGTCVKVLKALKEVA-EAAAEQHA 522
			RESULT 10
			AB46437
			ID AAB46437 standard; protein; 173 AA.
			XX
			AC AAB46437;
			XX
			DT 06-APR-2001 (first entry)
			XX
			DE C. purpureus delta6-acetylenase/delta6-desaturase SEQ ID NO 6.
			XX
			KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid; transgenic plant; plant oil; triglyceride; nutrition; animal feed; cosmetic.
			XX
			OS Ceratodon purpureus.
			PW WO2000075341-A1.
			XX
			PD 14-DEC-2000.
			XX
			PP 07-JUN-2000; 2000WO-EP005274.
			XX
			PR 07-JUN-1999; 99DE-01025718.
			PR 22-DEC-1999; 99DE-01062409.
			XX
			(BADI) BASF AG.
			XX
			Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;
			DR WPI; 2001-112150/12.
			DR N-PSDB; AAF25731.
			XX
			Nucleic acid encoding delta6-acetylenase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.
			PT
			PT
			XX
			Query Match 56.8%; Score 1475; DB 5; Length 525;
			Best Local Similarity 55.3%; Pred. No. 4e-147;
			Matches 281; Conservative 74; Mismatches 117; Irredundant 75; Gaps 6;

This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 178 aa or 172 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids

Query Match	Best Local Similarity	Score	DB	Length
Matched 173; Conservative 3;	100.0% ; Mismatches 0;	929;	4;	173;
		Pred. No.	7.1e-90;	
		Indels	0;	
		Gaps	0;	
251 IEHTAPNECDEQYTPLDEDIDTPIAWSKEILATVESKRILRVLQYQHYMILPILFEWAR				310
1 IEHTAPNECDEQYTPLDEDIDTPIAWSKEILATVESKRILRVLQYQHYMILPILFEWAR				60
311 YSWTFGSLLFTFNPDLSSTKGLIEKGTVAFHYAWFSWAFAHPGVAKPLAWMIVATELVA				370
61 YSWTFGSLLFTFNPDLSSTKGLIEKGTVAFHYAWFSWAFAHPGVAKPLAWMIVATELVA				120
371 GLLIGEVETLSHNGKEVYNESKDFEVRAQVITTRNTKRGWENDWETGGLDTQIE				423
121 GLLIGEVETLSHNGKEVYNESKDFEVRAQVITTRNTKRGWENDWETGGHDTOIE				173

SULT 11
984137 AFM64137 standard; protein; 457 AA.

AAW84137;
15-FEB-1999 (first entry)

A delta-6 desaturase enzyme.

Fatty acid; delta-6 desaturase; polyunsaturated fatty acid; malnutrition; inflammation; rheumatoid arthritis; asthma; psoriasis; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder

Mortierella alpina

卷之三

22 OCT 1998

סמלים וסודות במקרא

(CALJ) CALGENE LLC.
(ABBO) ABBOTT LAB.
Knutzon D, Mukerji P, Huang Y, Thurmond J, Chaudhary S;
Leonard AE;

WPI; 1998-594582/50.
N-PSDB; AAV63624.

New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed.

Claim 3: 319 3A-E; 165pp; English.

The present sequence represents a Mortierella alpina fatty acid delta-6 desaturase enzyme. The enzyme sequence is used in the methods of the invention. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. The present desaturase is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty acids. The enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit Platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastrointestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and inflammatory skin disorders.

Sequence 457 AA:

114 ATFHIPPAAWKQLNDYYIGDL---AREEPLDELLKDYRDMRAEFYREGLFKSSKAWFLLQT 170

171 LINPALFAASIAITICY--DKSYWAIVLSASILMGLFVQQCGWLAHDFLHQVFFENRTANSF 228
83 DIFHEPLAWELLENNFIVGIDEDSRALNDEAHLVAGNEELQDGELELQDGAEL

129 SENLICINGLSTVIVAKWGTSTLANVLSAALLIGLFWQQCGWLAAEDFLHHQVFQDRFWGDL 188

189 FGAFLGGVCGQFSSSWKDKHNTTHAAPNVAHGE-----DPDIDTHPLLTWSEHAELEMFSID 243

286 VESKRILRVLQYQHYMIL-----PILLEMARYSNTFGSSLFTFNPDLSTTK----- 330
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
244 VPDEELTRM-----WSBEMVYLNOTTWEYFILLSEFABLSWCTQOSILFEYI-----PNNGAHHKPSSGARYPT 309

331 GLIEKGTVAFFHYAWFSAAFFHILPGVAKPLAMWATELVAGLILLGFVFILSHNGKEVYNE 390

THE SILVER CLOUDS ARE IN THE SKY, AND THE VINES ARE SWAYING IN THE BREEZE.

391 SK---DEVARQVITTRNTRGENDWEIGGLDTQIEHHLEFTIMPRHNPKIAPOVEALC 446
362 EEAVDMDEFETKQIITGRDVHPGLFANWTFGLNYOLEHHLFPSMPRHNSKIQPAVETLC 420

447 KKHLGLEYDNVSVVGASVAVVKALKEIADEAS 477

RESULT 12
AAW95504
ID AAW95504 standard; peptide; 457 AA.
xx

essential FAs obtained can be used in nutritional formulations or animal feed formulations. The long chain PUFAs can be used in nutritional formulations, cosmetic formulations or animal feed formulations. The products can also be used for producing transgenic animals which can be used for producing essential FAs which can be used for producing downstream products such as leukotrienes, thromboxanes, arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. The products can also be used in cell culture. The animal or milk fat produced can be administered to treat malnutrition

essential FAs obtained can be used in nutritional formulations or animal feed formulations. The long chain PAs can be used in nutritional formulations, cosmetic formulations or animal feed formulations. The products can also be used for producing transgenic animals which can be used for producing essential PAs which can be used for producing downstream products such as leukotrienes, thromboxanes, arachidonic acid, eicosapentaenoic acid or docosahexaenoic acid. The products can also be used in cell culture. The animal or milk fat produced can be administered to treat malnutrition.

Sequence 457 AA;

Query Match	Score 841.5; DB 3; Length 457;
Best Local Similarity	39.2%; Pred. No. 6.3e-80;
Matches 177; Conservative	72; Mismatches 159; Indels 43; Gaps 10;
62 TYSLADV-----ASHDRPGDCWMIWKEKVVYDISRFADDHPGGTVISTYFGRDGTDFV 113	
9 TFRTRAEWLNAAEALNEGKKDAEAPELMIIDDNKVYDVREFVDPHGGSVILTHVGKDGTDFV 68	
114 ATFFPPPAWKQLNDYYIGDL---AREEPLDELLKDYRDMDRAEFVREGGLEFKSSKAWFLLOT 170	
69 ETFHPEAAWETLANFVYGVDDIDESDRDIKNDDEAAEVRLKLRTLFQSLGYDSSKAYYAFKV 128	
171 LINAALFAASIAATICY--DKSYWAIVLSSASLMLGFLVQQCGWLAHDFLHQVFEENRTANSF 228	
129 SFNLCLIWGLSTVWAKWGQTSTIANVLSSALLGEFQNQCGWLAHDFLHHHQVEQDRFWGDL 18B	
229 FGYLEFGNCVULGFSVSWRTRKNIHTAPNECDEQYTPLDEDIDTLPIIAWSK---EILAT 285	
189 FGAFIPEGWCQGFSSSWRKDKNTTHAAPPVHGE----DDPIDDTHPLITWSEHALEMESD 243	
286 VESKRILRVLQYQHYMIL----PLLEMARYSWTFGSLLFTFPNPDLSITK----- 330	
244 VPDEELTRM--WSRFMVNLNCTMFYFPILLSFARLSWCLQSILFVL-PNGQAHKPSSGARVPI 300	
331 GLIEKGTVAFHYAWFSSWAFFHILLPGVAKPLAAMVATELVAGLLLGFVFTLSHNGKEYVNE 390	
301 SLVEQLSLAMHWWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAZUFSSLNHNMGMPVISK 360	
391 SK----DFVRAQVETTRNTKRGWFDWFTGGLDTQIEHHLEPTMPRHNPYKTAPOQEALC 446	
361 EEAVDMDEFKQIITZGRDHPLGFLANFTGGLNYYQIEHHLPSPMRFNSKIQOPAVETLC 420	
447 KKHGLEYDNVSVVGASVAVVKALKEIADEAS 477	
421 KKYNVVERHETTGMIECTAEVFSRLLNEVSKAAS 451	

Query Match 32.4%; Score 841.5; DB 3; Length 457;

Best Local Similarity 39.2%; Pred. No. 6.3e-80;

Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 14;

Qy 62 TYSLADV-----ASHDRPGDCWMIWKEKVVYDISRFADDHPGGTVISTYFGRDGTDFV 113

Db 69 DTFHPEAAWETLANFVYGVDDIDESDRDIKNDDEAAEVRLKLRTLFQSLGYDSSKAYYAFKV 68

Qy 114 ATFFPPPAWKQLNDYYIGDL---AREEPLDELLKDYRDMDRAEFVREGGLEFKSSKAWFLLOT 170

Db 129 SFPNLCLIWGLSTVWAKWGQTSTIANVLSSALLGEFQNQCGWLAHDFLHHHQVFODRFWGDL 171

Qy 229 FGYLEFGNCVULGFSVSWRTRKNIHTAPNECDEQYTPLDEDIDTLPIIAWSK---EILAT 285

Db 189 FGAFLGGVCQGFSSSWRKDKNTTHAAPPVHGE----DDPIDDTHPLITWSEHALEMESD 243

Qy 286 VESKRILRVLQYQHYMIL----PLLEMARYSWTFGSLLFTFPNPDLSITK----- 311

Db 244 VPDEELTRM--WSRFMVNLNCTMFYFPILLSFARLSWCLQSILFVL-PNGQAHKPSSGARVPI 312

Qy 331 GLIEKGTVAFHYAWFSSWAFFHILLPGVAKPLAAMVATELVAGLLLGFVFTLSHNGKEYVNE 333

Db 313 Misc-difference 172. :176

Qy 314 /label= histidine_box /note= "conserved_among membrane-bound desaturases"

Key 315 Location/Qualifiers

Misc-difference 209. 213

delta-6 desaturase; gamma-linolenic acid; biosynthesis; transgenic insect cell; polyunsaturated long chain fatty acid; antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic; osteopathic; cytostatic; dermatological; gynecological; anti-HIV; neuroprotective; nephrotropic; vasodilator; antiaggregant; vasotropic.

Mortierella alpina.

10-AUG-2000 (First entry)

M. alpina delta-6 fatty acid desaturase.

AAY92599 standard; protein; 457 AA.

AAY92599

10-AUG-2000 (First entry)

M. alpina delta-6 fatty acid desaturase.

delta-6 desaturase; gamma-linolenic acid; biosynthesis; transgenic insect cell; polyunsaturated long chain fatty acid; antiinflammatory; antirheumatic; antiasthmatic; antipsoriatic; osteopathic; cytostatic; dermatological; gynecological; anti-HIV; neuroprotective; nephrotropic; vasodilator; antiaggregant; vasotropic.

Location/Qualifiers

Key 316 Misc-difference 172. :176

Qy 317 /label= histidine_box /note= "conserved_among membrane-bound desaturases"

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Db 301 SLVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMPVISK 360 Qy 171 LINAALEFAASIAATICY--DKSYWAIYVLASASLMGLFVOOCGWLADFLHQQVFENRTANSF 228 Qy 391 SK---DEVRAQVITTRNTKRGWFNDWETGGLDTQIEHHLFPTMPRHNPXPCLAPOVERALC 446 Db 129 SFNLICIWGLISTVIVAKWGTSTLAVVLSAIDLIGLFWQQCGWLADFLHQQVFQDRFAGDL 188 Db 361 EAVIDMDPFTKQIITGRDVHEGLFANWFTGGLNYQIEHHLFPSSMRHNFSKIQPAVETLC 420 Qy 229 FGYLFGNCVLFGFSVSWWRTKHNTHTHTAPNECDQXYTPLDEDIDTLPITIAWSK--EILAT 285 Db 189 FGAFLGGVCQGFSSSSWWKDKHNTHHAAPNVEGE---DPDIDTHPLLTWSEHALEMFSID 243 Db 447 KRKHGLEVDNVSVVGSAYVKALKELTADEAS 477 Qy 286 VESKRILRVLQYQHYMIL-----PLLFMARYSJWTFGSLLFTENPDLSSTK----- 330 Db 421 KRYNVRVYHTTGMIETGAEVFSRLINEVSKAAS 451 Qy 286 VESKRILRVLQYQHYMIL-----PLLFMARYSJWTFGSLLFTENPDLSSTK----- 330 Db 244 VPDEELTRM--WSRFMVNLNQTWFFYFPILSFARLSWCLOSILFVL-PNGQAHKPSGARVPI 300

RESULT 15

ID AAB31684 Standard; protein; 457 AA.

XX AAB31684;

AC AAB31684;

XX DT 30-APR-2002 (First entry)

XX Amino acid sequence of a fungal delta6 desaturase.

XX XX delta6 desaturase; desaturase gene; elongase gene; fatty acid; eicosanoid; nutrition; infant formula; dietary supplement; dietary substitute; animal feed.

XX OS *Yarrowieella alpina*.

XX PN WO200104636-A1.

XX PD 18-JAN-2001.

XX PF 11-UTJL-2000; 20000WO-US019011.

XX PR 12-UJUL-1999; 99US-00351525.

XX PA (UYOH-) UNIV OHIO.

XX PI Kopchick JJ, Kelder B;

XX DR 2001-182622/18.

XX DR N-PSDB; AAF25234.

PT New compositions comprising cells that express desaturases and elongases, for synthesizing essential fatty acids or long-chain polyunsaturated fatty acids, used in nutritional, cosmetic or animal feed formulations.

XX Disclosure; Fig 9; 93pp; English.

CC The present sequence represents a delta6 desaturase. The desaturase polynucleotide sequence was used to transfet mammalian cells, to produce animal cells expressing a desaturase gene and/or an elongase gene.

CC Compositions comprising cells of the invention are useful for synthesising essential fatty acids, their derivatives or downstream products, as well as altered levels of long-chain polyunsaturated fatty acids and eicosanoids. The compositions are useful in nutritional formulae, e.g. infant formula, dietary supplements or dietary substitutes for both humans and animals. The compositions are also useful in cosmetic or animal feed formulations. Furthermore, the compositions may also be used as fat free media or as research reagents

XX Sequence 457 AA;

Query Match 32-4%; Score 841.5; DB 4; Length 457;

Best Local Similarity 39.2%; Pred. No. 6.3e-80;

Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

Qy 62 TYSLADV-----ASHDRPGDGCWMIIVKEYVYDISRFAADDHPGGTVISTYFRGDGTDF 113

Db 9 TTTTAAVLMNAEALNEGKKAQDAEAPPFLMIDNKVYDVREFVDPDHGGSVILTHVGKDGTDF 68

Qy 114 ATFHPPAAWKQLNDYIGDL--AREEPIDELLKTDYRDMAAEFVREGLEFKSSKAWELLQT 170

Db 69 ETFHPEAAWETLANFYVGDIIDESDRDIKNDFAAEVRKLRTLFOQSUGYDSSKAYYAFKV 128

Sequence 17, Appl
 Sequence 11, Appl
 Sequence 199828, A
 Sequence 48669, A
 Sequence 13, Appl
 Sequence 20, Appl
 Sequence 5, Appl
 Sequence 5, Appl
 Sequence 69, Appl
 Sequence 22, Appl
 Sequence 4, Appl
 Sequence 3, Appl
 Sequence 12, Appl
 Sequence 447, APP
 Sequence 279631, A
 Sequence 52563, A
 Sequence 1240, AP
 Sequence 6108, AP
 Sequence 42, Appl
 Sequence 9, Appl
 Sequence 38, Appl
 Sequence 7, Appl
 Sequence 26, Appl
 Sequence 8, Appl
 Sequence 3, Appl
 Sequence 27, Appl
 Sequence 1, Appl
 Sequence 1301, AP
 Sequence 6, Appl

 23.7 323 14 US-10-191-513A-17
 23.3 603.5 14 US-10-340-779A-11
 22.6 587 14 US-10-424-599-299828
 22.6 587 12 US-10-425-114-4B669
 22.1 574 14 US-10-340-779A-13
 21.8 567 14 US-10-340-779A-20
 21.8 567 13 US-10-029-756-5
 21.8 567 16 US-10-702-777-5
 21.8 567 16 US-10-231-956A-69
 21.2 549 12 US-10-429-160-22
 21.2 549 12 US-10-415-232-4
 21.2 549 14 US-10-262-617-3
 21.1 547 14 US-10-191-513A-12
 21.0 546 14 US-10-389-566-447
 21.0 546 16 US-10-424-599-179631
 20.9 542 12 US-10-425-114-52563
 20.9 542 12 US-10-296-115-1240
 20.8 539 12 US-10-369-493-6108
 20.6 535 15 US-10-191-513A-42
 20.6 534.5 14 US-10-191-513A-9
 20.5 532.5 14 US-10-191-513A-38
 20.3 528 12 US-10-239-652A-7
 20.3 444 16 US-10-429-160-25
 20.3 528 12 US-10-239-652A-8
 20.3 528 16 US-10-415-232-3
 20.1 521 13 US-10-029-756-27
 20.1 452 16 US-10-702-777-27
 19.8 445 14 US-10-262-617-1
 19.8 490 12 US-10-296-115-1301
 19.7 473 12 US-10-239-652A-6

 615 23.7 : Protein search, using sw model
 603.5 : run on: June 16, 2004, 19:05:56 ; Search time 49 Seconds
 587 : (without alignments)
 587 : 2777.015 Million cell updates/sec

 Perfect score: 2595
 Sequence: - MALVTFNFIGTTNSKYSV.....AVVKALKEIIDEASIRLFAH 483

 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

 Searched: 1158786 segs, 281726120 residues
 Total number of hits satisfying chosen parameters: 1158786

 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Published Applications AA; *
 Database: *

SUMMARIES							
Result No.	Score	Query Match Length	DB ID	Description			
1	1475	56.8	525	12 US-10-250-821-8	Sequence 8, Appli	QY	1 MALVTDLNFGLTT---WSKYSVYTHSYAGNYGPTLKHKKVS
2	1475	56.8	525	12 US-10-250-821-27	Sequence 27, Appli	Db	25 MSLFSDFFPSVSSSTVGWSVHSIQPLK-----RITSKKRVSESAVQCRNSS 77
3	1475	56.8	525	12 US-10-250-821-30	Sequence 30, Appli	QY	41 -----AQGKTAGOTLRQRWSQDKKPGTYSLADVASHDRPGDCWWIVKEKVYDLSRFADD 94
4	1475	56.8	525	12 US-10-250-553-8	Sequence 8, Appli	Db	78 TQTAEALAESVVKPTRLSSQWKK-STHPLSEVAVHNKPSDCWIVVKNKVYDVSNFADE 136
5	1475	56.8	525	12 US-10-250-553-27	Sequence 27, Appli	QY	95 HPGGGTIVSTYFGRDGTDPATFHPPAAWKOLNDYYIGDLAREEPLDELILKDYRDMRAEFV 154
6	1475	56.8	525	12 US-10-250-553-30	GENERAL INFORMATION	Db	137 HPGGSVISTYFGRDGTDFVSSFHAASTWKILQDFYIGDVERVEPTPELLKOFREMRAEL 136
7	841.5	32.4	457	14 US-10-278-391-4	Sequence 4, Appli	QY	155 REGFKSSKAWFLLQTLINAAFLFAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 214
8	841.5	32.4	458	14 US-10-191-513A-12	Sequence 11, Appli	Db	138 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 256
9	841.5	32.4	458	14 US-10-191-513A-41	Sequence 41, Appli	QY	139 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 214
10	799.5	30.8	477	12 US-10-250-821-4	Sequence 4, Appli	Db	140 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 256
11	799.5	30.8	477	12 US-10-250-553-4	Sequence 4, Appli	QY	141 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 214
12	798.5	30.8	453	10 US-C9-769-863-14	Sequence 14, Appli	Db	142 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 256
13	798.5	30.8	453	14 US-10-054-534B-14	Sequence 14, Appli	QY	143 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 214
14	798.5	30.8	453	14 US-10-431-952-14	Sequence 14, Appli	Db	144 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 256
15	798.5	30.8	453	14 US-10-054-534B-14	Sequence 8, Appli	QY	145 RQLEFKSSKLYYYVMKLLTNVAIFAAASIACTYDKSYWAVLSSASLMLGFLVQQCGWLHDF 214

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match: 56.8%; Score 1475; DB 12; Length 525;
 Best Local Similarity 55.3%; Pred. No. 4e-14.6;
 Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;

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  1 MALVTDLFNLFGLT---WSKYSVYTHSYAGNYGPTLKHKVSV-
  25 MSLFSDFSYVSSTWGSWSVSHSIQPLK-----RLTSKRVSESAAVQCISSAEVQRNSS 77
  41 ----AOGKTAGQTLLRQRSPVQDKKKPGTYSLADAVASHDRPGDCWMIVKEKYDISRFADD 94
  78 TQGTAAELAESVVVKPTTRRSSQWKK-STHPLSEAVHNKPSPDCWIVVVKNVYDVSNFADE 136
  QY 95 HPGGTIVISTYEGRDGTDVFAEFPAAWKOLNDYYIGDOLAREEPDLIELKDYRDMDRAEFV 154
  Db 137 HPGGSV-VISTYEGRDGTDVSSFEHAASSTWKILQDFYIIGDVERVEP-PELLKDREMALLEL 196
  QY 155 REGLFKSKRAWELLQTLINAAFLPAAASIATICDKSYWVNLISASLMGLFVQQCGWLAHDF 214
  Db 197 REQLFKSKLYYYMKLLTNVAAFAASIAIICWSRTISAVLASACMMALCFQCGWLSHDF 256
  QY 215 LHQQVFENRTANSFEGGYLGNCYLGFSVSWWRTKHNIHHTAPNECDEQYTPLDDEDIDTLP 274
  Db 257 LHNQVFETRWLINEVGYVIGNAVLGSTGWKEGHNLHHAAPMECDQTYQPIDEDIDTLP 316
  QY 275 LIAWSKELATVESRRILRVLQYQHYMLPILLFMARYWTGSSLILFTNPDLSTTKGLIE 334
  Db 317 LIAWSKDDILATVENKTFLRILQYOHLEFFARGSWLFWSTRYTSTAVLSPVDRILLE 376
  QY 335 KGTVAFAHYAWFSWAFAHILPGVAKPLAMVATELVAGLLGIVFTLSHNGKEVYNESKDF 394
  Db 377 KGTVLFIYFWFVGTACYLPG-WKPLVWMAVTTELMSGMLIGFVFFVLSHNGMEVYNSSSKEF 435
  QY 395 VRAQVITTRNTKRGWENDWETGGLDTQZ-EHLEPFTM.RHNPYKIAPOVEALCKKHGLEID 454
  Db 436 VSAQIVSTRDIGNIFNDWFETGGLNRIEHHLFPTMPRHNLINKIAPRVEFCKKHGLYE 495
  QY 455 NWSVVGASVAVVKALKERIAADEPSIRLHA 482
  Db 496 DVSIAATGTCVKVLKALKEVAA-EEAAEQHA 522
  
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RESULT 7
 US-10-278-391-4
 Sequence 4, Application US/10278391
 Publication No. US20030159164A1
 GENERAL INFORMATION:
 APPLICANT: KOPCHIK, JOHN J.
 KELDER, BRUCE
 HUANG, YUNG-SHENH
 KIRCHNER, STEPHEN J.
 MUKERJI, PRADIP
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 SYNTHESIS OF FATTY ACIDS, THEIR DERIVATIVES AND DOWNSTREAM
 PRODUCTS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 MONTGOMERY STREET, SUITE 2200
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/278, 391
 FILING DATE: 23-Oct-2002
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/087, 578

FILING DATE: 29-MAY-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: CARROLL, PETER G.
 REGISTRATION NUMBER: 32, 837
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 457 amino acids
 TYPE: amino acid
 STRANDEDNESS: No. US20030159164A1 Relevant
 TOPOLOGY: No. US20030159164A1 Relevant
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-10-278-391-4

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  Query Match 32.4%; Score 841.5; DB 14; Length 457;
  Best Local Similarity 39.2%; Pred. No. 2.1e-79;
  Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;
  
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  62 TYSLADV-----ASHDRP3DCWMMIVKERVYDISRADDHPGGTVISTYFGRDGDTDVF 113
  9 TFRABEVNLNAEAALNEGKKADEAEPFLMIIDNKVYDVREFVPEHPGGSVILTHVGKDGTDVF 68
  114 ATFHPPAAWKQOLNDYYIGDL-----AREEPLDELLKDYRDMDRAEFVREGLFKSSKAWFLLOT 170
  69 DTFHPERAWEETLANFYVGIDESSRDIKNDDEPAEVRKRLTLFQSLSGYDSSKAYYAFKV 128
  171 LINNALFAASIAITCY-DKSYWAIILSASLMGLFVQQCGWLAHDFLHQVFEENRTANSF 228
  129 SFNLCIWGLSTVIAKMGQTSTLAVNLSAALLGLFWQQCGWLAHDFLHQVFDWFGLD 188
  229 FGYLEFGNCVULGF SVSWWRTKHNIHHTAPNECDEQYTPLDDEDIDTLP.LIAWSK-----DPDIDTHPLLTWEHALEMFSD 243
  189 FGAFLGGVCOGESSSWWDOKHNTNHAAPNVEGE-----DPDIDTHPLLTWEHALEMFSD 243
  286 VESKRILRVLQYQHYML-----PLLEMARYSWTFGSSLFTFPDLSTTK-----330
  244 VPDEELTRM--WSRETVLNQTWYFPILSPEARLSWCQSLTFLFVLPNGQAEHKPSGARVPI 300
  
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  331 GLIEKGTVAFHYAWFSWAFAHILPGVAKPLAMVATELVAGLLGIVFTLSHNGKEVYNE 390
  301 SILVEQLSLLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNHNGMVPISK 360
  
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  391 SK-----DFVRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNPYKIAPOVEAALC 446
  361 EAVIDMDFFTKQIITGRDVFHVGPLEFPMSPMRHNEISKIQPAVETLC 420
  
```

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  447 KKHGLEYDNVSVVGSVAVVKALKETADEAS 477
  421 KKNVRYRHTTGMIEGTAEVFSRNLNEVSKAAS 451
  
```

RESULT 8
 US-10-191-513A-11
 Sequence 12, Application US/10191513A
 Publication No. US20030104596A1
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pardip
 ; APPLICANT: Leonard, Amanda E.
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Tapas, Das
 ; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
 ; FILE REFERENCE: 6295-US.D3
 ; CURRENT APPLICATION NUMBER: US/10/191,513A
 ; CURRENT FILING DATE: 2002-09-25
 ; PRIOR APPLICATION NUMBER: US 09/227,613
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: PCT/US98/07422
 ; PRIOR FILING DATE: 1998-04-10

PRIOR APPLICATION NUMBER: US 08/833,610
PRIOR FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 11
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (458) .. (458)
OTHER INFORMATION: Xaa = Unknown or other at position 458
US-10-191-513A-41

Query Match 32.4%; Score 841.5; DB 14; Length 458;
Best Local Similarity 39.2%; Pred. No. 2.1e-79;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

Query Match 32.4%; Score 841.5; DB 14; Length 458;
Best Local Similarity 39.2%; Pred. No. 2.1e-79;
Matches 177; Conservative 72; Mismatches 159; Indels 43; Gaps 10;

Qy 62 TYSLADV-----ASHDPRPGDCWMIIVKEKVDYDISREADDHPGGTWISTYFGRDGTDVF 113
Db 9 DTFRAEVLAEEALNEGGKDAEAPFLMIDDNKVYDVREFVPDFHPGGSVILTHVGKDGTDFV 68

Qy 114 ATFHPPAAWKQLNDYYIGDL--AREEPLDELLKDYRDMRAEFVREGLFKSSKAWEFLQQT 170
Db 69 DTFHPEAAWETLANFYVGDIEDSDRDIIKNDFAAEVRKLRTLQSLGGYDSSKAYYAFKV 128

Qy 171 LINAALFAASIAATICY--DKSYWATVLSSASLMGLEWOOCGWLAHDFLHQOVFENRTANSF 228
Db 129 SFNLCIWGLSTVIVAKWGOTSTLAVNLSSAALLGLFWQQCGWLAHDFLHQVDFRWGDL 188

Qy 229 FGYLFGNCVLGFSVSWRTKHNTHHTAPNECDEQYTPLDEDIDTLPILLAWSK---EILAT 285
Db 189 FGAFLGGVCGFSSSSWWKDKHNTTHAAPNVAHGE----DPDIDTHPLLTSEHALEMFS 243

Qy 286 VESKRILRLVQYQHML-----PLLFMARRYAWFSAAFHILPVGAKPLAMVATEVAGLLIGFVFTLSHNGKEVYNE 330
Db 244 VPDEELTRM--WSREMVLNOTWFFYFPILSFARLSWCLQSILFV--PNGQAHKPSGARVPI 300

Qy 331 GLIEKGTVAFHYAWFSAAFHILPVGAKPLAMVATEVAGLLIGFVFTLSHNGKEVYNE 390
Db 301 SILVEQLSLAMHWTWYLATMFLFIKDPVNMLVYFLVSQAVCGNLLAIVFSLNNGMPVIISK 360

Qy 391 SK----DFVRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNPKIAQVEALC 446
Db 361 EEAVIDMDEFITKQIITGRDVHPLGANWFTGGLNYQIEHHLFPSMMPRHNSKIQPAVETLC 420

Qy 447 KKHGLEYDNVSVVGASAVVKALKETADEAS 477
Db 421 KKYNVRHTTGMIEGTAEVFSRNLNEVSKAAS 451

RESULT 10
US-10-250-821-4
Sequence 4, Application US/10250621
Publication No. US20040049805A1

GENERAL INFORMATION:
APPLICANT: BASF Plant Science GmbH
TITLE OF INVENTION: Method for the Expression of Biosynthetic Genes
TITLE OF INVENTION: in Plant Seeds Using Multiple Expression Constructs
FILE REFERENCE: 2000-904
CURRENT APPLICATION NUMBER: US/10/250,821
CURRENT FILING DATE: 2003-07-07
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin vers. 2.0
SEQ ID NO: 4
LENGTH: 477
TYPE: PRT
ORGANISM: Phaeodactylum tricornutum
US-10-250-821-4

Query Match 30.8%; Score 799.5; DB 12; Length 477;
Best Local Similarity 36.7%; Pred. No. 6e-75;
Matches 177; Conservative 73; Mismatches 162; Indels 71; Gaps 15;

Qy 40 SAQGKTAGQTLRORSVQDDKKPKGTYSLADJWASHDRPGDCWMIVKEKYDISRADDHPGGT 99
Db 9 ASKGSTAARKI-----SWEVKTHASPEDAWIHSNKVYDVSNW-HEHPGGA 54

QY 100 VISTYFGRDGTDVFAATEHPPAAWQQLNDYYIGDLARE---EPLD-ELLKDYRDMRAEFV 154
 Db 55 VIFTHAGDDMTDIFAAFPAPGSOSLMLKKFYIGELLPTTGGKE2QIAFERGYRDRLRSKLI 114

QY 155 REGLEFKSSKAWEFLLTQTLINAAALFAASIAATICYDKSYWAIVSLASLMGLFVQOCGWNLAHDF 214
 Db 115 MMGMFMSNKWFWYVYKCLSNMMAIWAACALVFSDRFWHLASAVMLGTFFQQSGWNLAHDF 174

QY 215 LHQQVFENRTANSFFGYLFGNCVLCVLFQWRKHNIIHTAPN-ECDEQYT-PLDEDIDT 272
 Db 175 LHHQVFTRKHGDLLGGLFWGNLMOGYSVQWWKXNKHNGHHAVPNLLHCSSAVALQDGDPPDT 234

QY 273 LPPIAWS-----KEILATVESKRILR-VLQYOHYMLPILLFMARYSW-----TFFGS 317
 Db 235 MPLLAWSVQQAQSYYRELQDGFKSLNMAIWAACALVFSDRFWHLASAVMLGTFFQQSGWNLAHDF 174

QY 318 LLFTENPDLS-TTKG----LIEKGTVAFHYAW-----TFFGS 317
 Db 295 GAASENAALELKAKGLQYPLLEKAGILLHYAWMLTVSSGEGRFSFAYTFYFILTATAS-- 352

QY 361 AWMVATELVAGLLGEVFTLSENGKEVYNES-KDFVRAQVITTRNTKRGW-----ENDW 413
 Db 353 -----CGFLLAIVEGLGLNGMATIN2DARPDFWKLQVTTTRNVTGGHGFQAFVDW 403

QY 414 FTGGIDTCIEHHLFPTMPRHNYPKIAPOWEALCKKHGLEYDNWSVGASVAVVKALKELA 473
 Db 404 FCGGLQYQVDDHHLFPSLPRHNLAKTHALVESFCKEWGVQYHEADLVDGTMEVLHHLGSSVA 463

QY 474 DE 475
 Db 464 GE 465

RESULT 11
 US-10-250-553-4
 ; Sequence 4; Application US/10250553
 ; Publication No. US20040053379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BASE Plant Science GmbH
 ; TITLE OF INVENTION: Production of polyunsaturated fatty acids, novel
 ; TITLE OF INVENTION: biosynthesis genes, and novel plant expression
 ; TITLE OF INVENTION: constructs
 ; FILE REFERENCE: 2000-873
 ; CURRENT APPLICATION NUMBER: US/10/250,553
 ; CURRENT FILING DATE: 2003-07-02
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Vers. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 477
 ; TYPE: PRT
 ; ORGANISM: Phaeodactylum tricornutum
 ; US-10-250-553-4

Query Match Score 799.5; DB 12; Length 477;
 Best Local Similarity 36.7%; Pred. No. 6e-75;
 Matches 177; Conservative 73; Mismatches 161; Indels 71; Gaps 15;

QY 40 SAQGKTAGTQLRQRSVQDKKKPGTYSLADVASHDRPGDCWMIVKEKYVDISRFADDHPGGT 99
 9 ASKGSTAARKI-----SWQEVKTHASPEDAWIHSNKVYDWSNW-HEHPGGA 54

QY 100 VISTYFGRDGTDVFAATEHPPAAWQQLNDYYIGDLARE---EPLD-ELLKDYRDMRAEFV 154
 Db 55 VIFTHAGDDMTDIFAAFPAPGSOSLMLKKFYIGELLPTTGGKE2QIAFERGYRDRLRSKLI 114

QY 155 REGLEFKSSKAWEFLLTQTLINAAALFAASIAATICYDKSYWAIVSLASLMGLFVQOCGWNLAHDF 214
 Db 115 MMGMFMSNKWFWYVYKCLSNMMAIWAACALVFSDRFWHLASAVMLGTFFQQSGWNLAHDF 174

QY 215 LHQQVFENRTANSFFGYLFGNCVLCVLFQWRKHNIIHTAPN-ECDEQYT-PLDEDIDT 272
 Db 175 LHHQVFTRKHGDLLGGLFWGNLMOGYSVQWWKXNKHNGHHAVPNLLHCSSAVALQDGDPPDT 234

QY 273 LPPIAWS-----KEILATVESKRILR-VLQYOHYMLPILLFMARYSW-----TFFGS 317
 Db 235 MPLLAWSVQQAQSYYRELQDGFKSLNMAIWAACALVFSDRFWHLASAVMLGTFFQQSGWNLAHDF 294

QY 318 LLFTENPDLS-TTKG----LIEKGTVAFHYAW-----TFFGS 317
 Db 295 GAASENAALELKAKGLQYPLLEKAGILLHYAWMLTVSSGEGRFSFAYTFYFILTATAS-- 352

QY 361 AWMVATELVAGLLGEVFTLSENGKEVYNES-KDFVRAQVITTRNTKRGW-----ENDW 413
 Db 353 -----CGFLLAIVEGLGLNGMATIN2DARPDFWKLQVTTTRNVTGGHGFQAFVDW 403

QY 414 FTGGIDTCIEHHLFPTMPRHNYPKIAPOWEALCKKHGLEYDNWSVGASVAVVKALKELA 473
 Db 404 FCGGLQYQVDDHHLFPSLPRHNLAKTHALVESFCKEWGVQYHEADLVDGTMEVLHHLGSSVA 463

QY 474 DE 475
 Db 464 GE 465

RESULT 12
 US-09-769-863-14
 ; Sequence 14; Application US/09769863
 ; Publication No. US2003015714A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763.US.01
 ; CURRENT APPLICATION NUMBER: US/09/769,863
 ; CURRENT FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolegnia diclina
 ; US-09-769-863-14

Query Match Score 798.5; DB 10; Length 453;
 Best Local Similarity 37.9%; Pred. No. 7e-75;
 Matches 170; Conservative 74; Mismatches 173; Indels 31; Gaps 9;

QY 55 VQDKKKPGTYSLADVASHDRPGDCWMIVKEKYVDISRFADDHPGGTIVSTYFGRDGTDWFA 114
 Db 2 VQGQKAEKISWATIREHNRQDNAWIVIHHKVYDISAF-EDHPGGVVMFTQAGEDATDAFA 60

QY 115 TFHPEAAWQQLNDYYIGDLAR-----EEPLDELLKDYRDMRAEFVREGLFRS 161
 Db 61 VFHPSSAELKLEQYYVGDVDQSTAADVTSISDEVKKSQSDFIASYRKLRLEVRLGLYDS 120

QY 162 SKLYLYKCASTLSIALVSAAICLHFDSIATMIVAAVILGLFYQQCGWLAHDLHQVFE 221
 Db 121 SKLYLYKCASTLSIALVSAAICLHFDSIATMIVAAVILGLFYQQCGWLAHDLHQVFE 180

QY 222 NRTANSFFGYLFGNCVLGESVSWMRKTKHNIHTAPNECDEQYTPL-----DEBDIDTLPLI 276
 Db 181 NHLFGDLVGMVGNLWQGESVQWWQWIKHNTTHAIPN--LHATPEIAFHGDPDIDTMPL 237

QY 277 AWS-KEILATVESKRILRVLQYOHYMLPILLFMARYSWTFFGSLLFTF---NPDLSTK-- 330
 Db 238 AWSLRMAQHADSPVGLFEMRYQAYLYFPILLFARISWVIQSAMYAFYINVGPGBTEDRVQ 297

QY 331 -GLIEKGTVAFHYAWSWAFAEFLPGVAKPLAWNATELVAGLLGFVFTLSHNGKEYVN 389

Db 298 YPLLERAGULLYGGNNGLVYAAANMSLQAAAFLFLVSOASCGLFLIAVFSVGHNGTEVFD 357

QY 390 -ESK-DFRAQVITTEKRGWENDWFTGGIDTQIEHHLFPTMPRHNPKIAPOVEALCK 447
 : :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 358 KDSKPDPFWKLQLSTRNVTSSLWIDWFMGGGLNYQIDHHLFPMPVRHNLPALNVKSCLK 417

QY 448 KHGLEYDNVVVGASVAVVKALKELIADE 475
 : :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 418 QYDIPYHETGFIAGMAEVVWHLERISIE 445

RESULT 13
 US-10-054-534B-14
 ; Sequence 14, Application US/10054534B
 ; Publication No. US2003016752A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763-US-01
 ; CURRENT APPLICATION NUMBER: US/10/431,952
 ; CURRENT FILING DATE: 2003-05-08
 ; PRIOR APPLICATION NUMBER: US/09/769, B63
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolegnia diclina
 US-10-431-952-14

Query Match 30.8%; Score 798.5; DB 14; Length 453;
 Best Local Similarity 37.9%; Pred. No. 7e-75;
 Matches 170; Conservative 74; Mismatches 173; Indels 31; Gaps 9;

Qy 55 VQDKKPGTYSLADVASHDRPDCWMIVKEKYDISRFAADDHPGGTVISTYFGRDGTDVFA 114
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 2 VQGQKAEKISWATIREHNRODNAWIVHHKYDISAF-EDHPGGVVMFTQAGEDATAFA 60

Qy 115 TFHPPAAWKQNLNDYYIGDLAR-----EEPLDELLKDYRDMDRAEFVREGLFKS 161
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 61 VFHPSSALKLLEQYIYFGVDQSTAAVDTSISDEVKKSQSDPIASYRKLRLEVRLGLYDS 120

Qy 162 SKAWFLLQTLLNAIFPLASIATICDKSYWAIIVSLASLMLGFVQOCGWLAHDELHQVFE 221
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 121 SKLYYLKCASTLSIALVSAAICLHDSTAMMVAAVILGLFYQOCGWLAHDELHQVFE 180

Qy 222 NRTANSFFGYLGNCVNGLFWQWRTHNHTAPNECDEQYTPL---DEDIDTLPII 276
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 181 NHLFGDLVGVMMVGNLWQGFSVQWWKHNTHAIPN---LHATPEIAFHGDPPDIDTMPL 237

Qy 277 AWS-KEILLATESKRILRVLQYQHYMILPLLFMARYSWTFGSLLFTF---NPDLSTTK-- 330
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 238 AWSLKMAQHADSPWGLFFMFRYQAYLYFPILLFARISWVIQSAMYAFYNVGPGBTEDKVC 297

Qy 331 -GLIEKGTVAFHYWAAFHILPGVAKPLAMWVATELVAGLLGFVFTLSHNGKEVN 389
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 298 YPLLERAGILLYGGNLGLVYAAANMSLLQAAAFLEVSOASCGLFLAMVFSV3HNGMEVFD 357

Qy 390 -ESK-DFVRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNPKIAPOVEALCK 447
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 358 KDSKPDPFWKLQLSTRNVTSSLWIDWFMGGGLNYQIDHHLFPMPVRHNLPALNVKSCLK 417

Qy 448 KHGLEYDNVVVGASVAVVKALKELIADE 475
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 Db 418 QYDIPYHETGFIAGMAEVVWHLERISIE 445

RESULT 14, Application US/10431952
 Publication No. US2003019073A1
 GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Mukerji, Pradip
 ; APPLICANT: Huang, Yung-Sheng
 ; APPLICANT: Das, Tapas
 ; APPLICANT: Thurmond, Jennifer
 ; APPLICANT: Pereira, Suzette L.
 ; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
 ; FILE REFERENCE: 6763-US-01
 ; CURRENT APPLICATION NUMBER: US/10/431,952
 ; CURRENT FILING DATE: 2003-05-08
 ; PRIOR APPLICATION NUMBER: US/09/769, B63
 ; PRIOR FILING DATE: 2001-01-25
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14
 ; LENGTH: 453
 ; TYPE: PRT
 ; ORGANISM: Saprolegnia diclina
 US-10-431-952-14

Query Match 30.8%; Score 798.5; DB 14; Length 453;
 Best Local Similarity 37.9%; Pred. No. 7e-75;
 Matches 170; Conservative 74; Mismatches 173; Indels 31; Gaps 9;

Qy 55 VQDKKPGTYSLADVASHDRPDCWMIVKEKYDISRFAADDHPGGTVISTYFGRDGTDVFA 114
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 2 VQGQKAEKISWATIREHNRODNAWIVHHKYDISAF-EDHPGGVVMFTQAGEDATAFA 60

Qy 115 TFHPPAAWKQNLNDYYIGDLAR-----EEPLDELLKDYRDMDRAEFVREGLFKS 161
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 61 VFHPSSALKLLEQYIYFGVDQSTAAVDTSISDEVKKSQSDPIASYRKLRLEVRLGLYDS 120

Qy 162 SKAWFLLQTLLNAIFPLASIATICDKSYWAIIVSLASLMLGFVQOCGWLAHDELHQVFE 221
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 121 SKLYYLKCASTLSIALVSAAICLHDSTAMMVAAVILGLFYQOCGWLAHDELHQVFE 180

Qy 222 NRTANSFFGYLGNCVNGLFWQWRTHNHTAPNECDEQYTPL---DEDIDTLPII 276
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 181 NHLFGDLVGVMMVGNLWQGFSVQWWKHNTHAIPN---LHATPEIAFHGDPPDIDTMPL 237

Qy 277 AWS-KEILLATESKRILRVLQYQHYMILPLLFMARYSWTFGSLLFTF---NPDLSTTK-- 330
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 238 AWSLKMAQHADSPWGLFFMFRYQAYLYFPILLFARISWVIQSAMYAFYNVGPGBTEDKVC 297

Qy 331 -GLIEKGTVAFHYWAAFHILPGVAKPLAMWVATELVAGLLGFVFTLSHNGKEVN 389
 :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 298 YPLLERAGILLYGGNLGLVYAAANMSLLQAAAFLEVSOASCGLFLAMVFSV3HNGMEVFD 357

Qy 390 -ESK-DFVRAQVITTRNTKRGWENDWFTGGLDTQIEHHLFPTMPRHNPKIAPOVEALCK 447
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 Db 358 KDSKPDPFWKLQLSTRNVTSSLWIDWFMGGGLNYQIDHHLFPMPVRHNLPALNVKSCLK 417

Qy 448 KHGLEYDNVVVGASVAVVKALKELIADE 475
 : :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 418 QYDIPYHETGFIAGMAEVVWHLERISIE 445

RESULT 15
 US-09-967-477B-8

Sequence 8, Application US/09967477B
 ; Patent No. US20020156254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xiao Qiu
 ; APPLICANT: Haiping Hong
 ; TITLE OF INVENTION: FAD4, FAD5, FAD5-2, AND FAD6, NOVEL
 ; TITLE OF INVENTION: FATTY ACID DESATURASE FAMILY MEMBERS AND USES THEREOF
 ; FILE REFERENCE: BNZ-001
 ; CURRENT APPLICATION NUMBER: US/09/967,477B
 ; CURRENT FILING DATE: 2002-04-16
 ; PRIOR APPLICATION NUMBER: 60/236,303

RESULT 14
 US-10-431-952-14

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; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/297,562
; PRIOR FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Thraustochytrium sp.
JS-09-967-477B-8

Query Match 33.4%; Score 790; DB 9; Length 459;
Best Local Similarity 38.3%; Pred. No. 5.7e-14;
Matches 175; Conservative 69; Mismatches 167; Indels 46; Gaps 12;

Qy      57 DKKPGTYSIA---DWASHDRPGDCWMIIVREKVYDISRFADDHPEGTVISTYGRDGTDF 113
Db       3 DLKPGVKRIVSWKEIREHATPATWIVIHKVYDISKW-DSHPGGSVMLTOAGEDATDAF 61

Qy      114 ATEHPPAAWKOLNQYYIGDL-----AREEPLDELLKQYDMRAEFVVR 155
Db       62 AVFHPSSAKLKLIEQFYVGDVDETSKAELIEGERPASDEERARRERRINBEFLASHRIRVKKG 121

Qy      156 EGLFKSSK---AWFELLQTLINEALFAASIAATICYDKSYWAIVLSASIMGLFVOCQCGWLH 212
Db       122 MGLYDASALLYAWKLVSTEGIARVL--SMAICFFNSFAMYMVAGVIMGLFYCQSGWLH 178

Qy      213 DFLHQVFENRTANSFFGYLGFSVSVWWRTKHNTHHTAPN---ECDEQYTPLDED 269
Db       179 DFLHNQVCENRTLGNLIGCLNGNAWQGFSVQWWKHNHLHAVPNLHSAKDEGPIG-DDD 237

Qy      270 IDTLPIIAWSKEIL-ATVESKRILRLVLYQOHYMLPILMARYSWTEGSLLIFTNPDLST 328
Db       238 IDTMPLIAWSKEMARKAFESHHGPPFIRNQAFLYFPILLARLSQLAQSFFYVFT--EF 294

Qy      329 TKGLI----EKGTVAFHYAWFSAAFHILPGYAKPLAMVATELYAGLLLGFVETL 380
Db       295 SEGFIDKVEFDGPEKAGLIVHITYIWQLAIPFCNMMSLFEGVAYFLMGQASCGILLALVFSI 354

Qy      381 SHNGKEY-NESK-DFVRAQVITTRNTKRGWENDWFTGGLDQIEHHLFPTMPREHNPK 438
Db       355 SHNGMSVYERETKPDFWQLQWTTRNIRASVEMDWFTGGLNYQIDHHLFPLVPRHNLPKV 414

Qy      439 A2QVEALCKKHGLEYDNVVVGASVAVKALKEIADE 475
Db       415 NVLIKSCLKEFDIIPFHETGFWEIXEVWDHEADISKE 451

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Search completed: June 16, 2004, 19:09:42
 Job time : 51 secs

GenCore version 5.1.6
 Copyright (c; 1993 - 2004 Computer Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 18, 2004, 22:56:20 ; Search time 592 Seconds

(without alignments)
 3466.013 Million cell updates/sec

Title: US-09-980-468-2
 Perfect score: 2595
 Sequence: MALVTDLNFEGTNSKYSV.....AVVKALKEIADEASIRLHAAH 483

Scoring table:

BLOSUM62	Xgapop 10.0	Xgapext 0.5
	Ygapop 10.0	Ygapext 0.5
	Fgapext 7.0	
	Delop 6.0	Delext 7.0

Searched:

3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 Command line parameters:
 -MODE=frame+P2n.model1 -DEV=x1h
 -Q=/cgn2_1/USPTO_spool/US09980468/runat_16062004_174741_27165/app_query.fasta_1.647
 -DB=N_Geneset_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=3.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blossum62 -TRANS=human40.cdi
 -LIST=45 -DOALIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pcto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US09980468 @cgn_1.1.470 @runat_16062004_174741_27165 -NCPU=6 -ICPU=3
 -NO_MPAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -DELEXT=7
 -FGAPEXT=7 -YGAPCP=10 -YGAPEXT=0.5 -DELCP=6 -DELOP=6

RESULT 1
 ID AAF25730 standard; DNA; 1467 BP.

XX AAF25730;
 AC
 XX DT 06-APR-2001 (first entry)

XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 3.
 XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
 XX transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic; ds.
 XX OS Ceratodon purpureus.
 XX PN WO200075341-A1.
 XX PD 14-DEC-2000.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2595	100.0	1467	4	AAF25730		Aaf25730 C. purpur
2	2595	100.0	2040	4	AAF25729		Aaf25729 C. purpur
3	1619	62.4	2160	4	AAF25734		Aaf25734 C. purpur
4	1475	56.8	1578	6	ABV74260		Abv74260 Physcomit
5	1475	56.8	1578	6	ABQ76782		Abq76782 P. patens
6	1475	56.8	2012	4	AAF26040		Aaf26040 P. patens
7	1475	56.8	2012	7	ABX13450		Abx13450 P. patens
8	1475	56.8	15430	6	ABV74274		Abv74274 Plant spe

%
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries

Result 1
 ID AAF25730 standard; DNA; 1467 BP.

XX Key Location/Qualifiers
 10..1461 CDS
 /*tag= a /product= "delta6-acetylenase/delta6-desaturase"

XX PN WO200075341-A1.
 XX PD 14-DEC-2000.
 XX PP 07-JUN-2000; 2000WO-EP005274.
 XX PR 07-JUN-1999; 99DE-01025718.
 XX PR 22-DEC-1999; 99DE-01062409.
 XX PA (BADI) BASF AG.

PI	Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;	QY	161 SerSerLysAlaLysPheLeuLeuGlnThrLeuIleAsnAlaAlaLeuPheAlaAlaSer 180
XX	WPI; 2001-112150/12.	DB	490 AGTCCAAAGCCTGGTTCAGCTCTGTTAAATGCAGCTCTTGCTGGAGC 549
DR	P-PSDB; AAB46436.	QY	181 IleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleValLeuSerAlaSerLeuMet 200
XX	Nucleic acid encoding delta6-acetyl enase or desaturase, useful for producing plant oils with increased content of unsaturated fatty acids.	DB	550 ATTGCGACTATCGTTCAGCAAGAGTTACTGGSTATTTGCTGGCAGCTTGATG 609
PS	Claim 1a; Page 46-48; 63pp; German.	QY	201 GlyLeuIeValGlnCysGlnCysGlyTrpLeuAlaHisAspPheLeuHisGlnGlnValPhe 220
XX	This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetyl enase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I); (E) or the vectors of (c); (e) Preparation of unsaturated fatty acids (A) or triglycerides (TG) with increased content of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A) or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids	DB	610 GGTCTCTGTCACAGTCGCTGGATGGCTGCTGGTTCATCAACAGGCTTT 669
CC	Sequence 1467 BP; 356 A; 349 C; 379 G; 383 T; 0 U; 0 Other;	QY	221 GluAsnArgThrAlaAsnSerPhePheGlyTrpLeuPheGlyAsnCysValLeuGlyPhe 240
CC	DB	670 GACACCGTAACCGGAACCTCCCTTGGCTATTGGCTATTGGCAATTGGCAATTGGCTGGCTTT 729	
CC	DB	241 SerValSerTrpTrpArgThrLysHisAsnIleHisHisThrAlaProAsnGluCysAsp 260	
CC	DB	730 AGGTGATCATGGGAGGGACGACATTCACTCATACTGCTCGAAATGAGTGGTGCAGC 789	
CC	QY	261 GluGlnTrpTrpProLeuAspGluAspPheLeuPheLeuProIleAlaTrpSerLys 280	
CC	DB	790 GAACAGTACACACCTCTAGACGAAGACATTGATACTCTCCCCATCATGGCTGGAGCAAG 849	
CC	QY	281 GluIleLeuIaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHistYR 300	
CC	DB	850 GAAATTGGCCACCCGGTAGAGGAACGAAAGGAAACAGTGTGCTTCAATATCAGCTAC 909	
CC	QY	301 MetIleLeuProLeuLeuPheMetAlaArgTyrrSerTrpTrpPheGlySerIleLeuPhe 320	
CC	DB	910 ATGATTCTGCCCTCATATGGTTCAAGTGGTCAAGTTGGACTTTGCAAGTTGGCTCTTC 969	
SQ	Alignment Scores:	QY	321 ThrPheAsnProAspLeuSerThrThrLysGlyLeuIleArgValLeuGlnTyrGlnHistYR 340
DB	Pred. No. : 2.2e-284	QY	340 .
DB	Score: 2595.00	DB	970 AGCTTCAATCCCTGATTGAGCTGACCAAGGAAACAGTGTGCTTT 1029
DB	Percent Similarity: 100.00%	QY	341 HisTrpTrpHeserTrpAlaAlaPheHisIleLeuProGlyValAlaLysProLeu 360
DB	Best Local Similarity: 100.00%	DB	1030 CACTACGCCCTGGTTCAAGTGGCTCCATATTTGCCGGTGTGGCTGGTCAAGCTCTT 1089
DB	Query Match: 4	DB	
DB	DB:	QY	361 AlaTrpMetValAlaThrGluLeuValAlaGlyLeuIleLeuGlyLeuAspThrLeu 380
DB	QY	1090 GCGTGGATGGCAACTGAGCTTGGCCGGTTCTGGGATTCGTTGTTACGTTG 1149	
DB	DB	381 SerHisAsnGlyLysGluValTyrProThrIleLeuProGlyValAlaLysProLeu 400	
DB	DB	1150 AGTCACAATGGAAAGGAGTTAACATIGAATGAAGGACTCTGTGAGAGGCCAGGTATT 1209	
DB	QY	401 ThrThrAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThr 420	
DB	DB	1210 ACCACCCGTAAACCCAAGGAGTTAACATIGAATGAAGGACTCTGTGAGAGGCCAGGTATT 1269	
DB	QY	421 GluIleGluHisIleLeuPheProThrMetProArgHisAsnTyrProLysIleAlaPro 440	
DB	DB	1270 CAGATTGAGCATCACCTGTTCCACAATGCCAGGCACAACTCCAAAGATGCACCT 1329	
DB	QY	441 GlnValGluAlaIleCysLysSlysHisGlyIleuGlutYrAspAsnValSerValGly 460	
DB	DB	1330 CAGGGTCAGGCTCTTGCAGAAAGCAGGGCTCGAGTAGGATATGGTCTCGTGTGGTGGT 1389	
DB	QY	461 AlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeu 480	
DB	DB	1390 GCCTCTGTCGAGCTTGCAGACGCTGGACCCCTGGAGGGACGGTA 1449	
DB	QY	481 HisAlaHis 483	
DB	DB	1450 CACGCTCAC 1458	
DB	RESULT 2		
DB	AAF25729		
DB	ID AAF25729 standard; DNA; 2040 BP.		
DB	XX		
DB	AC		
QY	141 GluLeuIeLysAspTyrArgAspMetArgAlaGluPheValArgGlyLeuPhyLys 160		
DB	370 GCATGGAACTCAATGAGCTAACAGAGATATGAGGCCAGTGGTGTAGAGAAGGGCTTTCAAG 489		
QY	430 GAATTGCTTAAGACTACAGAGATATGAGGCCAGTGGTGTAGAGAAGGGCTTTCAAG 489		

Db 1316 AGTCACAATGGAAACGGAGGTACAATGAAAGCAGCTTCGTGAGGCCAGGTATT 1375
 Qy 401 ThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyLeuAspThr 420
 Db 1376 ACCACCGTAACCTAGCGAGGCTGGTTCAACGATTGGTCAACTGGGAACCTCGACACC 1435
 Qy 421 GlnIleGluHisIleLeuPheProThrMetProArgHisAsnTyProLySileAlaPro 440
 Db 1436 CAGATTGAGCATACCTGTTCAACATGCCAGGCCACAACATACCCAAGATCGCACCT 1495
 Qy 441 GlnValGluAlaLeuCysLysIleGluGlyLeuGluItyAspAsnValSerValValGly 460
 Db 1496 CAGGTCTGGCTCTTGCAAGAACGGCAGCCGGCTCGAGTACGATRGTCTCCGTGCTGGT 1555
 Qy 461 AlaSerValAlaValValLysGluIleAlaAspGluAlaSerIleArgLeu 480
 Db 1556 GCCTCTGTGCGGTRGTGTAAGGAAATTGCTGTATGAAGCGTCATTGGCTT 1615
 Qy 481 HisAlaHis 483
 Db 1616 CACGGTCAC 1624

RESULT 3
 AAF25734 standard; DNA; 2160 BP.
 ID AAF25734 ;
 XX DT 06-APR-2001 (first entry)
 XX DE C. purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 11.
 XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;
 KW transgenic plant; plant oil; triglyceride; nutrition; animal feed;
 KW cosmetic; ds.
 XX OS Ceratodon purpureus.
 XX Key Location/Qualifiers
 FT CDS 159 . 1721
 FT /*tag= a /product= "delta6-acetylenase/delta6-desaturase"
 FT PN WO2000075341-A1.
 XX PD 14-DEC-2000.
 XX PF 07-JUN-2000; 2000WO-EP005274 .
 XX PR 07-JUN-1999; 99DE-01025718 .
 PR 22-DEC-1999; 99DE-01062409 .
 XX PA (BADI) BASF AG.
 XX PI Heinz B, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;
 XX DR WPI; 2001-112150/12 .
 DR P-PSDB; AAB46440 .
 XX PT Nucleic acid encoding delta6-acetylenase or desaturase, useful for
 producing plant oils with increased content of unsaturated fatty acids.
 XX PS Claim 1a: Page 54-57; 69pp; German.
 XX This invention describes a novel isolated nucleic acid (I) encoding
 CC polypeptides (II) with Delta6-acetylenase and/or Deltad6-desaturase
 CC activity. The invention also describes (a) amino acid sequences encoded
 CC by (I); (b) an expression cassette (EC) containing (I) linked to one or
 CC more regulatory sequences; (c) a vector containing (I) and EC; (d)
 CC organisms containing (I), EC or the vectors of (c); (e) preparation of
 CC unsaturated fatty acids (A) or triglycerides (TG) with increased content
 CC of (A) by introducing (I) or EC into an oil-producing organism; (f)
 CC proteins (IIa) of 172 aa or 178 aa (given in the specification); (g)

CC production of (A) or TG by using (Ia); and (h) (A) and TG produced by
 CC method (g). (I) are used to produce transgenic plants (or other
 CC organisms) that produce oils or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and/or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and/or triglycerides (TG) with increased content
 CC of unsaturated fatty acids (A) and/or triglycerides (TG) containing them, are useful in human
 CC homology screening. (A), or TG containing them, are useful in human
 CC nutrition (e.g. infant foods), animal feeds, pharmaceuticals and
 CC cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can
 CC be used to suppress expression of (II), resulting in oils with increased
 CC content of saturated fatty acids
 XX SQ Sequence 2160 BP; 509 A; 481 C; 556 G; 614 T; 0 U; 0 Other;
 XX Alignment Scores:
 Pred. No.: 3.39e-173 Length: 2160
 Score: 1619.00 Matches: 302
 Percent Similarity: 76.17% Conservative: 72
 Best Local Similarity: 61.51% Mismatches: 101
 Query Match: 62.39% Indels: 16
 DB: 4 Gaps: 3
 US-09-980-468-2 (1-483) x AAF25734 (1-2160)
 Qy 1 XetAlaLeuValThrAspPheLeuGlyThrThrTrpSerLysThrSerVal 20
 Db 231 ATGCCCTCTGTCACTGACTTCCTRAATGTCCTGGAAACGACTTGGGCACTGGACTCTT 290
 Qy 21 TyrThrHisSerTyraAlaGlyAsnTyrGlyProThrLeuLysLysValSer 40
 Db 291 TCCACT--ACATTCGCTTTCAAGAGGCTCACGACTAAAGAACACAGTTGCCACATCTG 347
 Qy 41 AlaGln----GlyLysThrAla 46
 Db 348 GTGGAGGCACANLAAGAATCGGTTGGCGGCCAGTGGAGATATTCTCAATCGGTT 407
 Qy 47 GlyGlnThrLeuArgGlnArgSerValGlnAspLysLysProGlyThrTyrSerLeuAla 66
 Db 408 GCGCAGCCCATCAGGGGAGGGTGGTCAGGATTAAGGATLAGCGGTTACTTACAGCTGAAG 467
 Qy 67 AspValAlaSerHisAspArgProGlyAspPhiSProGlyGlyThrValIleSerThrTyrPheGly 106
 Db 468 GATGTAGCTTCGACAGATAATGCCAGGACTGCTGGATATAATCAAAGAGAAAGGTGTAT 527
 Qy 87 AspIleSerArgPheAlaAspAspPhiSProGlyGlyThrValIleSerThrTyrPheGly 106
 Db 528 GATGTAGCCACCTTCGCTGAGGAGGACCCACCTTATCAACACCTACTTCGGAA 587
 Qy 107 ArgAspGlyThrAspValPheAlaThrPheHisProProAlaAlaTrrPheGlyLeuAsn 126
 Db 588 CGAGACGCCACAGATGGTTCCTCTACTTTCCACGCATCCACCTCATGGAGATTCCTCAG 647
 Qy 127 AspTyrTyrIleGlyAspLeuAlaArgGluProLeuAspGluLeuLeuAsn 146
 Db 648 ATTTCCTACATCGGGAAACCTTGTAGGGAGGAGCCGACTTTGGCAAGAGCTTCCAATCTACTAC 767
 Qy 147 ArgAspMetArgAlaGluPheValLeuLeuLeuLeuLeuLeuAsn 166
 Db 708 AGAGAGTTGAGGCCCTTTCTGAGAGAACAGCTTCAAGAGTTCCAATCTACTAC 767
 Qy 167 LeuLeuGlnThrLeuIleAspAlaAlaLeuPheAlaAlaSerIleAlaThrIleCystYr 186
 Db 768 CTTTCAACAGACTCTCATTAATGTTCCATTGTCGATAATCAGTCTG 827
 Qy 187 AspLysSerTyrTrpAlaIleValLeuSerLeuMetGlyLeuPheValGlnGln 206
 Db 828 TACAGTCTTACGGGGTCTCTGTATCAGCCAGTTGATGGGCTTATCAACACAG 887
 Qy 207 CYSGLYTIPLeAlaHisAspPheLeuHisGlnGlyAlaPheGluAsnArgThrAlaAsn 226
 Db 888 TGGGATGGTGTCTACGATTTCACCATCAGSTATTGAGCACAGCTGGCTCAAT 947
 Qy 227 SerPhePheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpPheArg 246
 Db 948 SACGTTGGCTATGGCTTCTGGATTCAACGTTGCTGGCAACGGCAACGTTGTTCTGAGTGGAAAG 1007

QY 247 ThrLysHisAsnIleHisthrAlaProAsnGluCysAspGluGlnTyrThrProLeu 266
 DB 1008 ACCAAGGCCAACCTGCATCATGGTGTGAAATGCGACCAAAAGTAGCACCCSRIT 1067

QY 267 AspGluAspIleAspThrLeuProIleLeuAlaIleLeuProLeu 286
 DB 1068 GATGAGGATATTGATACTCTCCCATCATGGCTCTGGAGTAAGATCTCTGGCCACTGTT 1127

QY 287 GluSerIysArgIleLeuIleGlnTyrGlnHistyrMetIleLeuProLeuLeu 306
 DB 1128 GAGAGCAAGGACCATGTCAGTTCAGTACCAAGCACCTATTCTTGGTTCTTTTG 1187

QY 307 PheMetAlaArgTyrSerTrpThrPheGlySerIleLeuPheThrAsnProAspLeu 326
 DB 1188 ACGTTTGCGCGGGCGAGTGGCTATTGGAGGCCCTTCACTCTCAGGCCGAGTTG 1247

QY 327 SerThrThrLysGlyLeuIleGluIysGlyThrValAlaPheHistyrAlaIlePheSer 346
 DB 1248 ACCCTTGGCGAGAACGTTGGAGGGAAACGATGGCTTGCACATTTGGTTAAT 1337

QY 347 TyrAlaAlaPheHisIleLeuProGlyValAlaLysProLeuAlaIleLeu 366
 DB 1308 AGTRGTRGTTTATCTGCRCCCAGA---TGGAAACCACTGTTGATGGGTTCAGC 1364

QY 367 GluLeuValAlaAlaGlyLeuIleGlyValPheThrLeuSerHisAsnGlyLysGlu 386
 DB 1365 GAGCTCATGTCGGTTCCTGGATACTGATTGGTACTCAGTCACAATGGATGGAG 1424

QY 387 ValTyrAsnGluUserLysAspPheValArgAlaGlnValIleThrThrArgAsnThrLys 406
 DB 1425 GTGTTACAATACGTCAGTCAAGGACTTCGGTGAATGCCAGATTGCACATCAA 1484

QY 407 ArgGlyTrpPheAsnAspPheValArgAlaGlnValIleThrThrArgAsnThrLys 426
 DB 1485 CGAGGGGTGTTAAATGATTGGTTCACAGACAGATTGAGCATCATCTA 1544

QY 427 PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeuCys 446
 DB 1545 TTTCACAAACGNTGGCCACGGCACACCTTAATAAAATTCTCAGCTGGAGACTTTGGTC 1604

QY 447 LysLysHisGlyLeuGluTyrAspAsnValSerValValGlyAlaSerValVal 466
 DB 1605 AAGAACGATGGACTGGCTTACGGAGACGTGAGCATGGCTTCCGGTTRIG 1664

QY 467 LysAlaLeuIysGluIleAlaAspGluAlaSer 477
 DB 1665 AAAACACTTGGACCTGGATGCCATGCTCA 1697

RESULT 4
 ID ABV74260 standard; CDNA; 1578 BP.
 XX ABV74260;
 DT 28-MAR-2003 (first entry)

DE Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
 KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
 KW gene; ss.

OS Physcomitrella patens encoding CDNA SEQ ID NO 7.

XX Location/Qualifiers
 FH 1..1578
 FT /tag= a
 /product= "desaturase"
 XX DE10102337-A1.
 PN 25-JUL-2002.
 PD 95 HisProGlyGlyTyrValIleSerThrTyrPheGlyArgAspGlyTyrAspValPheAla 114

XX 19-JAN-2001; 2001DE-01002337.
 PP
 XX PR
 XX PA (BADI) BASF PLANT SCI GMBH.
 XX PI Lerchl J., Renz K., Heinz E., Domerque F., Zaehringen U.;
 XX DR WPI; 2002-644810/70.
 DR P-PSDB; ABB98277.

PT Preparing ester containing polyunsaturated fatty acids, useful e.g. in animal or human nutrition, by transforming organism with desaturase gene from Phaeodactylum tricornutum.

XX PS Example 16; Page 60-63; 182pp; German.

XX The invention relates to preparing (MI); fatty acid esters (I) with an increased content of polyunsaturated fatty acids (II) with at least two double bonds by introducing into a (I)-producing organism a specific nucleic acid (A). (MI) is useful for preparing ester containing polyunsaturated fatty acids. Oils, lipids and (II) or their fractions, produced by (MI) are used in animal and human nutrition, cosmetics and pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. Cells that express (A) are also used to identify (ant) agonists of desaturases, e.g. for modulating the yield and rate of production of particular fine chemicals in microorganisms (claimed). Also (A) and derived proteins can be used as markers of specific genomic regions and in evolutionary/protein structural studies. (MI) is suitable for large scale production (no known bioengineering method can produce (II) on a useful scale). The present sequence is that of a Physcomitrella patens desaturase encoding cDNA used as the (A) component of the invention in producing transgenic (I) -

XX SQ Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 3 U; 0 Other;

XX Alignment Scores:
 Pred. No.: 4.9e-157 Length: 1578
 Score: 1475.00 Matches: 281
 Percent Similarity: 69.88% Conservative: 74
 Best Local Similarity: 55.31% Mismatches: 117
 Query Match: 56.84% Indels: 36
 DB: 6 Gaps: 6

JS-09-980-468-2 (1-483) x ABV74260 (1-1578)

QY 1 MetalAlaIleValThrAspPheLeuAsnPheLeuGlyLysThrThr-----TriPheSerLys 17
 DB 73 ATGTCCTCTCTCAGCGACTCTTCAGTTATGTTGCTTCACTGTTGTTCTGAGCGCTA 132

QY 18 TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
 DB 133 CACAGTATAACACCTTTGAAG 171

QY 38 LysValSer-----
 DB 172 CGTGTTCGGAAAGGGCTGCCGAAATGTTAGAGAAATTTCGAGT 231

QY 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgGlnArgSer 54
 DB 232 ACCAGGGAACTGGGGCAACTCGCGAATCGTGAAGCCCCAGGAGGGTCA 291

QY 55 ValGlnAspLysProGlyThrTyrSerLeuAlaAspValAlaSerHisAspArgPro 74
 DB 292 TCTCAGTGGAAAGG---TCGACACACCCCTATCAGAAAGTACACAAAGGCCA 348

QY 75 GlyAspCysTrpMetLysValTyrAspIleSerArgPheAlaAspAsp 94
 DB 349 AGCGATTGGCTGGATGTTGTTCAAAAAACAAGGTGTATGTTGCGGACGAG 408

Db	409	CATCCCGAGGATCAGTTATTAGTACTTATTGGACAGACGGCACAGATGTTCTCT	1486	GACGTATCTATTGCTACCGGCACITGCCAAGGTTTGAAAGCATTCAGGAAGTCGCG---	1542
QY	115	ThrPheHisProProAlaAlaTPILYSGlnLeuAsnAspTyrTyrIleGlyAspLeuAla	475	GluAlaSerIleArgLeuHisAla	482
Db	469	AGTTTCATGCTCTACATGGAAATATCTTCAGACTTTACATTGGTACAGTGGAG	1543	GAGGCTGCGGCAGAGCAGCATGCT	1566
QY	135	ArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArgAlaGluPheVal	154	ABQ76782 standard; cDNA;	1578 BP.
Db	529	AGGGTGGGCCGACTCCAGAGCTGCTGAGATTCCGAGAAATGAGGCTCTTCTCT	588	ABQ76782;	
QY	155	ArgGluGlyLeuPheLysserLysAlaTrpPheLeuGlnThrLeuIleAsnAla	174	RESULT 5	
Db	589	AGGGAGCAACTTICAAGGTTGAAATTGTAATTGTTACTATGTTATGAACTCGATGTT	648	ABQ76782	
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCystYrasPlysSertYrrTrpAlaIleVal	194	25-MAR-2003 (first entry)	
Db	642	GTATTTGCTGCGAGCAATTGAAATAATGTTGGAGCAGACTATTTCAGCGGGTTTG	708	DE patens D6 desaturase cDNA SEQ ID 7.	
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValIglnGlnCysGlyTriPheAlaHisAspPhe	214	Promoter; expression cassette; structural gene; plant; transgenic; linseed; fatty acid ester; polyunsaturated fatty acid; PUFA; cosmetic; animal nutrition; human nutrition; pharmaceutical; cholesterol; blood; heart disease; seed-specific; gene; ss.	
Db	709	GCTTCAGCTTGTATAKSP3GGCTCTGTTAACAGTGGGATGGCTATCCCATGATT	768	XX	
QY	215	LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly	234	XX	
Db	769	CTCCACAAATCAGGTTGAGACACGGCTGGTTAATGAAAGTGTGGGTATGTGATCGGC	828	Key	
QY	235	AsnCysvalLeuSlyEheservalSerTrpTrpArgThrLysHiAsnAlleHiShisThr	254	CDSS	
Db	829	AACGCCGTTCTG33CCTTAGTACAGGGTGGAAAGGAGAACATAACCTTCATCATGCT	888	1.: .1578	
QY	255	AlaProAlaGluCysAspGluGlnTyrThrProLeuAspGluAspTyrLeuPro	274	/* tag= a	
Db	889	GCTCCAAATGAAATGCGATCAGACTTACCAACCAATTGATGAAGATAATTGATGACTCTCCC	948	/product= "D6 desaturase"	
QY	275	IleIleAlaIrpSerLysGluIleLeuAlaIrpSerLysArgIleLeuArgVal	294	XX	
Db	949	CTCATTGCTGGAGCAAGGACATACTGGCACACAGTTGAGAATAAGACATTCCTGGAAATC	1008	{BADI } BASF PLANT SCI GMBH.	
QY	295	LeuGlyTyrGlnHistYrMetIleLeuProLeuPheMetAlaArgTyrSerTrpThr	314	XX	
Db	1009	CTCCAAATCAGCATCTGTTCTCATGGGCTGTTATTTTCGCCCCGGTGAATGGCTC	1068	Lerchl J, Duwenig E, Bischoff F, Heinz E, Drexler H, Scheffler J,	
QY	315	PheGlySerIleLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu	334	XX	
Db	1069	TTTGGAGCTGGGAGATAACCTCTACAGCAAGCTCTCACCTGTGACAGGGTTGGGAG	1128	WPI; 2002-675961/73.	
QY	335	JysGlyIleGlyValAlaPheHistYrAlaIrpPheSerTrpAlaAlaPheHistIleLeuPro	354	XX	
Db	1129	KGCGGAACCTGTTCTGTTCACTACTTTGTTCTGCTGGACAGCGTCTATCTCTCCCT	1188	DR; P-PSDB; ABG73602.	
QY	355	S-LysValAlaIlysProLeuAlaIrpMetValAlaThrGluLeuValAlaGlyLeuLeu	374	XX	
Db	1189	SGT--TGGAGCCATTAGTATGGATGGCGGTGACTGAGCTCATGTCGGATGCTGCTG	1245	XX	
QY	375	SlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe	394	This invention describes novel expression cassette (EC) containing at	
Db	1246	GGCTTGTGATTGTTACTTAGCCACAATGGATGGAGGTTATAATTCTGCTAAAGAAATC	1305	least one each of plant promoter (P) and structural gene (SG) expressed	
QY	395	ValArgAlaGlnValIleThrArgAsnThrLysArgGlyTrpPheAsnAspTyrPhe	414	in plants, flanked by specific restriction enzyme (RE) recognition sites.	
Db	1306	GTGAGTCACAGATCGTATCCACGGGATATCAAAACATATTCAACGACTGGTC	1365	The EC has the structure (L1-P-SC-L2) ⁿ where L1 = is a Polylinker (ABQ76798), L2 = any of three synthetic poly-linker-terminator-polylinker sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing sequences and n = 1-3. The invention discloses a vector containing this	
QY	415	ThrglyGlyLeuAspPheThrGlnIleGluHisIleLeuPheProThrMetProArgHisAsn	434	CC sequences, e.g. an organism containing the EC or the vector and a transgenic plant containing a (non-) functional nucleic acid in the vector. Transgenic plants e.g. linseed can be prepared with improved production of fatty acid esters with an increased content of polyunsaturated fatty acids (PUFA), useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g. PUFA are known to reduce levels of cholesterol in the blood and to protect against heart disease. The expression cassettes of the invention provide increased and more efficient production of fine chemicals (especially PUFA), including seed-specific production. This sequence represents a nucleic acid sequence used to illustrate the method of the invention	
Db	1366	ACTGGTGCCTAACAGGCAAAATAGCCAAATAGCCAAATAGCCAGGCATAT	1425	CC	
QY	435	TyrProLysIleAlaProGlnIwAlaLeuCysIlysLysLysIleGluTyrAsp	454	XX	
Db	1426	TTAAACAAATAGCCACCTAGGTGGAGGTCTCTGTAAGAAAACGGTCTGGTGTACGA	1485	Sequence 1578 BP; 406 A; 333 C; 404 G; 435 T; 0 U; 0 Other;	
QY	455	AsnValSerValGlyAlaSerValAlaValAlaLysAlaLeuLysGluIleAlaAsp	474	Alignment Scores:	
Db			Score:	4.9e-157	Length:
QY			Percent Similarity:	14.88%	Matches:
			Conservative:	74	Percent:

Production of unsaturated fatty acids, useful e.g. in nutrition, cosmetics or pharmaceuticals, in organisms transformed with *Physcomitrella patens* delta-6-desaturase nucleic acid.

Claim 1a; Page 38-41; 49pp; German.

This invention describes a novel preparation of unsaturated fatty acids (I) by introducing into an organism at least one isolated nucleic acid (II) that encodes a polypeptide (III) with Delta6-desaturase activity. Organisms that contain at least 1 wt.% (I), on total fatty acid content, are then selected. (II) is selected from: (a) a 2012 bp sequence (S1), defined in the specification, or its equivalents within the degeneracy of the genetic code; or (b) derivatives of the sequence of (a) that encode 525 amino acid polypeptide (S2), defined in the specification, or a polypeptide with at least 50% homology with (S2) and practically the same enzymatic activity. The invention also describes (1) transgenic organisms that contain (II); and (2) oils, lipids and fatty acids produced by the new method. The oils, lipids and fatty acids produced by the transformed organisms are used in human or animal nutrition, cosmetics, pharmaceuticals and agricultural chemicals. (III) can also be used, in vitro, for increasing the (I) content of triglycerides. The transgenic organisms have increased contents of (I), or of (II)-containing triglycerides particularly of gammalinolenic acid.

QY	155	ArgGluGlyLeuPheLysSerSerLysAlaSerIleAlaThrIleCystYrAspLysSerTyrTrpPheLeuLeuGlnThrLeuIleAsnAla	174
Db	907	AGGAGCAACTTTCAAAAGTCGAATTGTACTATGGCTACGGATGGCTTCTGCTTCAACAGTGGATGGCTATCCATGATT	966
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCystYrAspLysSerTyrTrpAlaIleVal	194
Db	967	GCTATTTTGCTGCCAGCATTCATGCAATTATGTTGGAGCAAGCTATTTCAGGGTTTG	1024
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTripleAlaHisAspPhe	214
Db	1027	GCTTCAGCTTGTATGGCTTCAACAGTGGATGGCTATCCATGATT	1086
QY	215	LeuHisGlnGlnValPheGluAsnDargThrAlaAsnSerPhePheGlyTyrLeuPheGly	234
Db	1087	CTCCACAAATCAGGTGTTGACACGGCTGGCTTAATGAAAGTTGTCGGGTATGTGATCGGC	1146
QY	235	AsnCysValLeuGlyPheSerValSerIleSerTrpTrpArgThrLysHisAsnIleHisThr	254
Db	1147	AACGCCGTTCTGGGTTAGTACAGGGTGSTGGAAAGGAAAGCATAACCTTCATCATGCT	1206
QY	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro	274
Db	1207	GCTCCAATGAATGCAACTTACCAACCAATTGATGAAGATAATTGATACTCTCCCC	1266
QY	275	IleIleAlaIleTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuIleArgVal	294
Db	1267	CTCATTGGCTGGAGCAAGGACATACTGGCCACAGTTGAGAATAAGACATTCTGGAAATC	1328
QY	295	LeuGlnItyrglnHistYrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpThr	314
Db	1327	CTCCCAATACCGCATCTGGTTCATGGGTCTGTTATTTCAGGGTCTGGTAGTTGGCTTC	1384
QY	315	PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu	334
Db	1387	TTTGGAGCTGGAGATAAACCTCTACAGCAGTGGCTCACCTGACAGGGTGTGGAG	1446
QY	335	LysGlyThrValAlaPheHistYralaTrpPheSerIleAlaAlaPheHisIleLeuPro	354
Db	1447	AAGGAACTGGTCTGGTTCACTACTTGGTGGACAGGGTGTGGCTATCTTCCT	1506
QY	355	GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu	374
Db	1507	GGT---TGGAAAGCCATTAGTAGTGGATGGCTGACTGAGCTCATGTCAGTGGCTG	1563
QY	375	GlyPheValPheIleSerHisAsnGlyLysGluValTYRAsnGluSerLysAspPhe	394
Db	1564	GGCTTTGTATTGTTGACTTAGCCACAAATGGGATGGGTTATAATTCTGTCATAAGAAATTTC	1623
QY	395	ValArgAlaGlnValIleThrThrArgAsnThrLysGluValTYRAsnGluSerLysAspTrpPhe	414
Db	1624	GTGAGTCACAGATCTGATCAGATCTGATCCACACGGGATATTCAGGAACATATTCAAACGACTGGTTC	1683
QY	415	ThrGlyGlyLeuAspThrGlnIleGluHiShisLeuPhePrcTrirMetProArgHiAsn	434
Db	1684	ACTGGTGGCCTTAACAGGCCAAATAGGCCAAATAGGCATCATCTTCCCACAAATGCCAGGGCTAAATCTGCTTAAGAAATTTC	1743
QY	435	TyrProLysIleAlaProGlnIleValGluAlaLeuCysLysLysGlyLeuGlutYrAsp	454
Db	1744	TTAACAAATAGCCACCTAGTGGAGGTGTGTTGTAAGAAACACGGTCTGGGTACGAA	1803
QY	455	AsnValSerValValValIleAlaValIleLysGluIleAlaAsp	474
Db	1804	GACGGTATCTATTGCTACCGGCACTTGCAGGGTGTGCTGAGTGAAGGAAGTCACTGAGCTTGTACGAA	1860
QY	475	GluAlaSerIleArgLeuHisAla	482
Db	1861	GAGGCTGGCCAGAGCAGCATGCT	1884

RESULT 7
ABX13450
ID ABX1
XX AC

QY	155	ArgGluGlyLeuPheLysSerSerLysAlaTrpPheLeuLeuGlnThrLeuIleAsnAla	174
Db	907	AGGGAGCAACTTTCAAAAGTCCGAATTGTACTATGTTATGAGCTGCTCACGAATGTT	966
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCystYrAspLysSerTyrTrpAlaIleVal	194
Db	967	GCTATTTTGCTGGCATTTGCAATATAATGTTGGAGCAAGACTATTTCAGGGTTTTG	1026
QY	195	LeuSerAlaSerLeuMetGlyLeuPheValGlnGlnCysGlyTrrpLeuAlaHisAspPhe	214
Db	1027	GCTTCAGCTTGATGSCCTGTGTTAACAGTGGGATGGCTATCCATGATT	1086
QY	215	LeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly	234
Db	1087	CTCCACAAATCAGGTGTTGAGACACGCTGGCTTAATGAAGTGTGGATATGTCATCGGC	1146
QY	235	AsnCysValleGlyPheSerIleSerTrpTrpArgThrLysHisAsnIleHisIleThr	254
Db	1147	AACGCCGTTCTGGGTTAGTACAGGGTGSTGGAAAGGAGAAGCATAACCTTCATCATGCT	1206
QY	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro	274
Db	1207	GCTCCAATGAAATGCAATTGCGGATCTAGACTTACCAACCAATTGATGAAGATAATTGATACTCCCC	1266
QY	275	IleIleAlaTrpSerLysGluIleLeuAlaThrValGluSerIlyArgIleLeuArgVal	294
Db	1267	CTCATTTGCCTGGAGCAAGGACATTACTGGCCACAGTTGAGAATAAGACATTCTTGCGAATC	1326
QY	295	LeuGlnTyrGlnHistYrMetIleLeuProLeuPheMetAlaArgTyrSerTrpThr	314
Db	1327	CTCCAATACCAGGCATCTGGTCTCTCATGGGTCTGTTATTTTCGCCCCGTGGTAGTTGGCTC	1386
QY	315	PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu	334
Db	1387	TTTGGAGCTGGAGATATACTCTACAGCAGTCTCACCTGACAGGTGTTGGAG	1446
QY	335	LysGlyThrValAlaPheHisTyrAlaIleTrpPheSerTrpAlaAlaPheHisIleLeuPro	354
Db	1447	AAGGGAAACTGTTCACTACTTTGGTGTACTTAGCCACAATGGGATGGACAGGGTCTAC	1506
QY	355	GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu	374
Db	1507	GGT--TGGAAAGCCATTAGTAGTATGGATGGCTGACTGAGCTCATGTCGGCATGGCTG	1563
QY	375	GlyPheValPheThrLeuSerHisAsnGlyLysGluValValYrasnGluSerLysAspPhe	394
Db	1564	GGCTTTGTATTGTGACTTAGCCACAATGGGATGGCTTATAATTGCGTCAAAGAACATTTC	1623
QY	395	ValArgAlaGlnIvalIleThrArgAsnThrIleBargGlyTrpPheAsnAspTrpPhe	414
Db	1624	GTGAGTGCACAGATCGTATCCACACGGGATATCAAGGAAACATATTCAACGGACTGGTTC	1683
QY	415	ThrGlyGlyLeuAspThrGlnIleGluHiShisLeuPheProThrMetProArgHiAsn	434
Db	1684	ACTGGTGGCCTAACAGGCAAAATAGGGCATCATCTTTCCCACAAATGCGTCAAAGAACATT	1743
QY	435	TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysHiShisGlyLeuGluTyRAsp	454
Db	1744	TTAACAAAATAGCACCTAGAGTGGAGGTGTTCTGTAAAGAAACAGGTCTGGTACGAA	1803
QY	455	AsnValSerIleAlaSerValAlaValValLysAlaLeuLysGluIleAlaAsp	474
Db	1804	GACGTATCTATTGCTACCGGCACACTTGCAGGGTCTGGTACGAA	-- 1860
QY	475	GluAlaSerIleArgLeuHisAla	482
Db	1861	GAGGCTGGGGCAAGGAGGCAATGCT	1864

DB	451	CACAGTATAACAACCTTTGAAG-----CGCTGACGGAGTAAGAG	489
DT	04-JUN-2003	(First entry)	
XX	P. patens delta6-acyl-lipid desaturase corresponding to Genbank AJ222980.		
DB	38	LysValSer-----	
QY	CGTGTTCGGAAAGCGCTGCCATTGAAAGTCAGAAATTGAGCT	549	
DB	490	CGTGTTCGGAAAGCGCTGCCATTGAAAGTCAGAAATTGAGCT	549
KW	Expression cassette; transgenic; promoter; LOX5; Plant; food production;		
KW	animal feed; seed; stress resistance; disease resistance; starch content;		
KW	lipid content; dormancy; fibre content; pharmaceutical production;		
KW	fine chemical production; sterile plant; vitamin; flavouring; perfume;		
KW	dye; cotyledon; embryonic tissue; stress factor; LOX; ds.		
XX	Physcomitrella patens.		
PN	DE13127882-A1.		
QX	12-JEC-2002.		
PD	11-JUN-2001; 2001DE-01027882.		
PP	11-JUN-2001; 2001DE-01027882.		
PR	11-JUN-2001; 2001DE-01027882.		
DB	{BADI} BASE PLANT SCI GMBH.		
QY	Bischoff F, Feussner I, Loyall LP;		
PI	WPI; 2003-279966/28.		
DR	PT	Cassette for expressing transgene, useful e.g. in production of	
PT	PT	pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene	
PT	PT	of Arabidopsis, provides cotyledon-specific expression.	
PA	Claim 5; Page: 28pp; German.		
PS	CC	This invention describes a novel cassette for the transgenic expression	
XXX	CC	of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis	
CC	CC	thaliana or deletion variants of the LOX5 promoter which are functionally	
CC	CC	linked to the nucleic acid of the invention. The cassette is used to	
CC	CC	prepare transgenic organisms, especially plants, for production of foods,	
CC	CC	animal feeds, seeds (including those with increased resistance to stress	
CC	CC	and disease, altered starch/lipid contents or dormancy, or altered fibre	
CC	CC	content), pharmaceuticals (especially antibodies, vaccines, enzymes and	
CC	CC	pharmaceutical proteins) and fine chemicals (especially enzymes,	
CC	CC	vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,	
CC	CC	perfumes and dyes), also to produce sterile plants. The LOX5 promoter	
CC	CC	provides strong and specific expression in cotyledons and/or other early	
CC	CC	embryonic tissue, so can degrade, or protect against, stress factors to	
CC	CC	which these tissues are particularly sensitive. Since cotyledons are the	
CC	CC	main storage organs of seeds, expressing transgenes in them produces	
CC	CC	targeted increases/modifications in nutritional value. Expression in the	
CC	CC	cotyledons is homogeneous, there are no side effects on other plant	
CC	CC	organs (pollen) and the promoter is functional in a wide variety of	
CC	CC	plants (ornamentals or crops). This sequence represents a nucleic acid	
CC	CC	sequence associated with the Arabidopsis thaliana LOX gene described in	
CC	CC	the disclosure of the invention	
SQ	Sequence 2012 BP; 482 A; 427 C; 553 G; 550 T; 3 U; 0 Other;		
DB	1267	CTCATGGCCTGGAGCAAGGACATACTGGCCACAGTGTGGAAATC	1326
Alignment Scores:			
Pred. No.:	7.08e-157	Length:	2012
Score:	1475.00	Matches:	281
Percent Similarity:	69.88%	Conservative:	74
Best Local Similarity:	55.31%	Mismatches:	117
Query Match:	56.84%	Indels:	36
DB:	7	Gaps:	6
QY	1 MetalateuvalThrAspPheLeuAsnPheLenglyThr-----TrpSerLys 17		
DB	391 ArgCTCTCTCTAGGGACTCTTCAACTGTTGGCTATGCTGCTGCTG	450	
QY	18 TyrSerValtyrThrHisSerTyrAlaGlyAsnTyrglyProThrLeuLysAlaLys 37		

QY 375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValItyAsnGluSerLysAspPhe 394
 DB 1564 GCGTTGATATTGTACTTAGCCACAATGGATGGGTTATAATTGGTCTAAAGAATTC 1623
 CC The invention relates to preparing (M1) fatty acid esters (I) with at least two
 CC increased content of polyunsaturated fatty acids (II) with at least two
 CC double bonds by introducing into a (I)-producing organism a specific
 CC nucleic acid (A). (M1) is useful for preparing ester containing specific
 CC polyunsaturated fatty acids. Oils, lipids and (II), or their fractions,
 CC produced by (M1) are used in animal and human nutrition, cosmetics and
 CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
 CC the blood and to protect against heart disease. Cells that express (A)
 CC are also used to identify (ant)agonists of desaturases, e.g. for
 CC modulating the yield and rate of production of particular fine chemicals
 CC in microorganisms (claimed). Also (A) and derived proteins can be used as
 CC markers of specific genomic regions and in evolutionary/protein
 CC structural studies. (M1) is suitable for large scale production (no known
 CC sequencing method can produce (II) on a useful scale). The present
 CC sequence is that of the pUC19 based plant specific expression vector
 CC (ABV74272) expressing the Physcomitrella patens elongase (ABB98278) and
 CC the Phaeodactylum tricornutum desaturase (ABB98277) of the invention.
 CC (updated on 07-AUG-2003 to correct OS field.)
 XX

QY 415 ThrGlyGlyLeuAspPTargLnnIleGluHisHisLeuPheProThrMetProArgHisAsn 434
 DB 1684 ACTGGTGCCCTAACGGCAAATAGGCCATCATCCTTCCCLACATGCCAGGCATAAT 1743
 QY 435 TyrProLysIleAlaProGlnValGluAlaLeuCysLysLysIleGlyLeuGluItyAsp 454
 DB 1744 TTAAACAAATAGCACCTAGACTGGAGGTGTTCTGTAAGAACACGGGTCCTGGTGTACGAA 1803
 QY 455 AsnValIserValValAlaSerValAlaValValAlaLysGluIleAlaAsp 474
 DB 1804 GAGCTATCTATTGCTACGGCACTTGCAAGGTTTGAAGCATTTGAAGGAAAGTCGCG--- 1860
 QY 475 GluAlaSerIleArgLeuHisAla 482
 DB 1861 GAGGCTCGGCAGAGGCATGCT 1884

RESULT 8
 ABV74274 ID ABV74274 standard; DNA; 15430 BP.
 XX AC ABV74274;
 XX DT 07-AUG-2003 (revised)
 DT 28-MAR-2003 (first entry)

DB Plant specific expression vector expressing desaturase SEQ ID NO 25.
 XX Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;
 KW animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic;
 KW plant; elongase; gene; ds.
 XX OS Phaeodactylum tricornutum.
 OS Physcomitrella patens.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers
 FH CDS .11543..12415
 FT /*tag= a
 FT /product= "elongase"
 FT /*note= "ABB98278"
 FT CDS .13313..14890
 FT /*tag= b
 FT /product= "desaturase"
 FT /*note= "ABB98277"
 XX DE10102337-A1.
 XX PD 25-JUL-2002.
 XX PN 19-JAN-2001; 2001DE-0102337.
 XX PR 19-JAN-2001; 2001DE-0102337.
 XX PA (BADI) BASF PLANT SCI GMBH.
 XX PI Lerchl J., Renz A., Heinz E., Domerque F., Zaehringen U;
 XX DR WPI; 2002-644810/70.
 DR P-PSDB; ABB98278 , ABB98277 .

DB Preparing ester containing polyunsaturated fatty acids, useful e.g. in
 PT animal or human nutrition, by transforming organism with desaturase gene
 PT from Phaeodactylum tricornutum.

XX Example 11; Page 136-150; 182pp; German.
 PS XX
 CC The invention relates to preparing (M1) fatty acid esters (I) with at least two
 CC increased content of polyunsaturated fatty acids (II) with at least two
 CC double bonds by introducing into a (I)-producing organism a specific
 CC nucleic acid (A). (M1) is useful for preparing ester containing specific
 CC polyunsaturated fatty acids. Oils, lipids and (II), or their fractions,
 CC produced by (M1) are used in animal and human nutrition, cosmetics and
 CC pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in
 CC the blood and to protect against heart disease. Cells that express (A)
 CC are also used to identify (ant)agonists of desaturases, e.g. for
 CC modulating the yield and rate of production of particular fine chemicals
 CC in microorganisms (claimed). Also (A) and derived proteins can be used as
 CC markers of specific genomic regions and in evolutionary/protein
 CC structural studies. (M1) is suitable for large scale production (no known
 CC sequencing method can produce (II) on a useful scale). The present
 CC sequence is that of the pUC19 based plant specific expression vector
 CC (ABV74272) expressing the Physcomitrella patens elongase (ABB98278) and
 CC the Phaeodactylum tricornutum desaturase (ABB98277) of the invention.
 CC (updated on 07-AUG-2003 to correct OS field.)
 XX SQ Sequence 15430 BP; 3733 A; 3826 C; 4153 G; 3718 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1 1.55e-155 Length: 15430
 Score: 1475.00 Matches: 281
 Percent Similarity: 69.88% Conservative: 74
 Best Local Similarity: 55.31% Mismatches: 117
 Query Match: 56.84% Indels: 36
 DB: 6 Gaps: 6

US-09-980-468-2 (1-483) x ABV74274 (1-15430)

QY 1 MetAlaIeuValThrAspPheLeuAsnPheLeuGlyThrThr----TrpSerLys 17
 DB 13385 ATGTCCTCTCTTCAGGACTTCAGTTATGTCGCTTCAGTTCACTGTTGCTGGAGCGTA 13444
 QY 18 TyrSerValTyrrThrIsSerrYrrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys 37
 DB 13445 CACAGTATAACACCTTGAAAG----CGCTGACGAGGTGAGAG 13483
 QY 38 LysValSer----- 40
 DB 13484 CGTGTTCGGAAAGGCTGGCTGGCAATATGTTACAGGAAATTGCTGGAGTCGAGT 13543
 QY 41 -----AlaGlnGlyLysThrAlaGlyGlnThrLeuIargGlnIargSer 54
 DB 13544 ACCCAGGGAACTGGGAACTGGGAAATCACTGGCAGAACGAAAGGTCA 13603
 QY 55 ValGlnAspLysSproGlyThrThrSerIleSerIleAlaAspValAlaSerHisAspArgPro 74
 DB 13604 TCTCAGTGGAGAAAG--TCGAACACACCCCCTATCAGAAGTAGCTACACAAAGCCA 13660
 QY 75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94
 DB 13661 AGCGATGGATGGATGTTGTAATTTGCAAAACAAAGGTGTGTTCCAAATTGCGGAGCGAG 13720
 QY 95 HisProGlyGlyThrValIleSerThrTyrPheGlyArgAspGlyThrAspValPheAla 114
 DB 13721 CATCCGGAGGATCACTTTATTAGTACTATTGCAAGATGTTCTCT 13780
 QY 115 ThrPheAspProAlaAlaTrpIleSerIleAspTyrIleGlyAspIleAla 134
 DB 13781 AGTTTTCATGCAGCTCTACATGGAAAATTCTCAAGACTTTACATTGGTACAGTGTGGAG 13840
 QY 135 ArgGluGlupProLeuAspGluLeuLeuLysAspTyrArgGluLupheVal 154
 DB 13841 AGGGTGGAGGCCGACTCAGAGCTCTACAGTGTGGATGAGCTCTTCCCTG 13900
 QY 155 ArgGluGlyLeuPheLysserLysAlaTrpPheLeuLeuIleAsnAla 174
 DB 13901 AGGGAGCAACTTTCAAAAGTTCAAATGCTACAGGAATGTATGAACTATGCTACAGGAATGTT 13960

		Y	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleVal 194
		Y	13961	GCTATTGCTGGAGCCATTGCAATAATGTTGGAGCAAGACTATTCAAGGGTTRIG 14020
		Y	195	IeuSerAlaSerIleMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPhe 214
		Y	14021	GCTTCAGCTTGCTCGGTACCAACTGGATGGCTATCCATGATT 14080
		Y	215	LeuHisGlnIleValPheGluLysArgThrAlaAsnSerPhePheGlyTyrLeuPheGly 234
		Y	14081	CTCCACAAATCAGGTGTTGAGCACGCTTAATGAAGCTGTGCTATGTGATCGGC 14140
		Y	235	AsnCysValLeuGlyPheSerValSerTrpArgThrLysAsnIleHisIleThr 254
	b	Y	14141	AACGCCCTCTGGGTTAGTACAGGGTCCAGGAAAGCATAACCTTCATCATGCT 14200
		Y	255	AlaProAsnGluCysAspGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
		Y	14201	GCTCCAATGAAATGGATCAGGACTTACCAACCATTGATGAGTATTGATACTCTCCCC 14260
		Y	275	IleIleAlaIlePheSerIleGluIleLeuAlaIleGluSerLysArgIleLeuArgVal 294
	b	Y	14261	CTCCAAATCCGCTGGAGCAGGACATACTGGCCACAGTTGAGAATAGACATTCTGGAAATC 14320
		Y	295	LeuGlnTyrglnHistYrMetIleIleLeuPheMetAlaArgTyrSerTrpThr 314
		Y	14321	CTCCAAATCCGCTGGAGCAGGACATCTGGTCTCATGGGTCTGACAGGGTTGGGCTC 14380
		Y	315	PheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
	b	Y	14381	TITGGAGCTGGAGATAAACCTCTACAGCAGTGTCTCACCTGTGCTCATGGCT 14440
		Y	335	LysGlyThrValAlaPheHistYrAlaTrp2heserTrpAlaAlaPheHisIleLeuPro 354
		Y	14441	AAGGGAACTGTTCTGTTCACTACTTTGGTTCTGGGACAGGGTGCCTCTTCCTCCCT 14500
		Y	355	GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaLysGlyLeuLeuLeu 374
	b	Y	14501	GGT---TGGAAAGCCATTAGTAGATGGATGGC3GTGACTGAGCTCATGGTCTCATGGCT 14557
		Y	375	GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394
		Y	14558	GGCTTGTGTTATTGTACTTAGCCACAATGGGATGGAGGTTATAATTCTGTCATAAGAATTTC 14617
		Y	395	ValArgGlnIvalIleThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPhe 414
		Y	14618	GTGAGTCACAGATCGTATCCACACGGGTTATCAAAGGAAACATATTCAACGACTGGTTC 14677
		Y	415	ThrIleGlyIleAspThrGlnIleGluIleLeuCysLysLysGlyLeuGlutYAsp 434
	b	Y	14678	ACT3GTGGCCCTAACAGGCAAATAGGCATCATCTTCCCAACAAATGCCAGGCATAAT 14737
		Y	435	TyrProLysIleAlaProGlnValIglAlaLeuCysLysLysGlyLeuGlutYAsp 454
		Y	14738	TTAACAAAATAGCCTAGAGTGGGGTCTGTTCTGGTGTACGAA 14797
		Y	455	AsnValSerValValGlyAlaSerValAlaValLysAlaLysGluIleAlaAsp 474
		Y	14798	GACGTATCTATTGCTACCGGCACCTTGCAAGGGTAAAGCATTTGAAAGGAAAGTCGGC--- 14854
		Y	475	GluAlaSerIleArgLeuHisAla 482
	b	Y	14855	GAGGCTGGGGCAGAGGCAGCATGCT 14878

QY	18	TyrSerValTyrThrHisSerTyrAlaGlyAsnTyrGlyProThrLeuLysHisAlaLys	37		Db	14501	GGT---TGGAAAGCCATTAGTAGATGGATGGGGCATGGCTCATGGCTGCGCTG 14557
Db	13445	CACAGTATAAACCTTGAAAG-----GGCTGACGAGTAAGTG 13483		QY	375	GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluUserLysAspPhe	394
QY	38	LysValSer-----	40		Db	14558	GGCTTGATTTGTACTTAGCCACAAATGGATGGAGTTATAATCGCTCTAAGAATT 14617
Db	13484	CGTGTTCGGAAAGGGCTGCCAATGTTACAGCTGAAGTCAGGMAATTGAGT 13543		QY	395	ValArgAlaGlnValLeuThrArgAsnThrLysArgGlyTyrPheAsnAspPhe	414
QY	41	-----AlaGlnGlyLysThrAlaGlyGlnThrLeuArgLnnArgSer	54		Db	14618	GTGAGTGCAACAGATGGTATCCACAGGGATATCAAGGAAACATATTCAHGACTGGTC 14677
Db	13544	ACCCAGGAAACTGGGAGGCACITCGCAGAATCACTCGTGAAGGCCAACGAGGTCA 13603		QY	415	ThrGlyGlyLeuAspPheThrGlnIleGluHisLeuPheProThrMetProArgHisAsn	434
QY	55	ValGlnAspLysLysProGlyThrTySerLeuAlaAspValAlaSerHisAspArgPro	74		Db	14678	ACTGGTGGCTTAACAGCCAAATAGGATCACATCTTCCAAACAATGCCAGGGCTAAAT 14737
Db	13604	TCTCACTGGAAAGG----TCGACACACCCCCTATCGAAAGTAGCAGTACACAAAGCCA 13663		QY	435	TyrProLysIleAlaProGlnValGluAlaLeuCysLysSlyBHiSglyLeuGluTyPheAsp	454
QY	75	GlyAspCysteTmetTleValLysGluLysValTyAspIleSerArgPheAlaAspAsp	94		Db	14738	TTRAAACAAAATAGGCACTAGAGTGGAGGTCTGGTCTGGTGTACGAA 14797
Db	13661	AGCGATGGTGGATGTTGTAACAAAGGTGTTGATGTTCCATTGTTGGACGAG 13723		QY	455	AsnValSerValValGlyAlaSerValAlaValValLysGluIleAlaAsp	474
QY	95	HisProGlyGlyThrValLeuSerThrTyPheGlyArgAspGlyThrAspValPheAla	114		Db	14798	GAAGTATCTATTGCTACCGGGCATTGCAAGGTTTGAAGATTGAAAGTGC 14854
Db	13721	CATCCCGAGGATCAGTTATTAGTACTTATTGTTGGACGAGGACAGGACAGATGTTTCCT 13780		QY	475	GluAlaSerIleArgLeuHisAla	482
QY	115	ThrPheHisProProAlaAlaIlePlysGlnIleuAsnAspTyrTyrIleGlyAspLeuAla	134		Db	14855	GAGGCTGCCCCAGAGGACAGCATGCT 14878
Db	13781	AGTTTTCATGGAGCTTCTACATGGAAAATTCTCAAGACTTTTACATTGGTGAAGTGGAG 13840					RESULT 10
QY	135	ArgGluGluProLeuAspGluLeuLeuLysAspTyrArgAspMetArgAlaGluPheVal	154		ABV74275	ABV74275 standard: DNA; 17752 BP.	
Db	13841	AGGGTGGAGCCGACTCCAGAGCTGCTGAAAGATTTCCGAGAAATGAGGCTCTTTCRCG 13900		ID	ABV74275	standard: DNA; 17752 BP.	
QY	155	ArgGluGluLeuPheLysSerSerLysAlaIlePheLeuIleGlnThrLeuIleAsnAla	174		XX	XX	
Db	13901	AGGGAGCACAACCTTTCAAAAGTTCGAAATTGACTATGTTATGAAAGCTGCTCACGAATGTT 13960		DT	07-AUG-2003	(revised)	
QY	175	AlaLeuPheAlaAlaSerIleAlaThrIleCysteSerTyrTyrPheAlaLeuIleAsnAla	194		XX	XX	
Db	13961	GCTATTGTTGCTGCGAGCATTTGCAATAATAATGTTGGAGCAGACTATTTCAGGGTTRTG 14020		DT	28-MAR-2003	(first entry)	
QY	195	LeuSerAlaSerIleMetGlyLeuPheValIglnGlnCysGlyTyrPheLeuAlaHisAspPhe	214		XX	XX	
Db	14021	GCTTCAGCTGTGTTGATGGCTCTGTGTTCCAAACASTGGATGGCTATCCCATGATTG 14080		KW	XX	Desaturase; fatty acid; ester; polyunsaturated fatty acid; cosmetic;	
QY	215	LeuHisGlnGlyPheGluAsnArgThrAlaAsnSerPhePheGlyTyrLeuPheGly	234		OS	animal nutrition; pharmaceutical; cholesterol; heart disease; transgenic; plant; elongase; gene; ds.	
Db	14081	CTCCACAAATCAGGGTGTGTTGAGACAGCTGCTATGAAAGTTGAGGATGGCTATCCCATGATTG 14140		OS	XX	Phaeodactylum tricornutum.	
QY	235	AsnCysValLeuGlyPheSerValSerTrpTrpArgThrLysHisAsnIleHisHisthr	254		Key	XX	Synthetic.
Db	14141	AACGCCGIRCTG3GTTTAGTACAGGGTGTGTTCAACASTGGCTTAATGAAAGTTGAGGATGGCTATCCCATGATTG 14200		CDS	11543	-12415	
QY	255	AlaProAsnGluCysAspGluGlnTyrTrpProLeuAspGluAspIleAspThrLeuPro	274		FT		/*tag= a
Db	14201	GCTCCAAATGAAATGGAATGGAATCTGACTTACCAATTGATGAAGATTGATACTCTCCC 14260		FT		/product= "elongase"	
QY	275	IleIleAlaIleIleLeuAlaIleThrValGluUserLysArgIleLeuArgVal	294		FT		/note= "ABB982278"
Db	14261	CTCATTGCGAACATACTGGCCACAGTTGAGAATAAGACATTGCGAATC 14320		FT		15791	-17200
QY	295	LeuGlnTyrGlnHistYzMetIleLeuProLeuLeuPheMetAlaArgTyrSerTriPhe	314		FT		/*tag= c
Db	14321	CTCCAAATACCGCATCTGTTCTCATGGGTCTGTTATTCGGCGTGGTAGTGGCTC 14380		FT		/product= "desaturase"	
QY	315	PheGlySerLeuLeuPheHistYzAlaPheHisIleLeuPro	334		FT		/note= "ABB982274"
Db	14381	CTTTCGAGCTGGAGATAACCTCTACAGGAGCTGCTTCACTTTCGGTGTGCTATCTTCRCCCT 14500		PR	19-JAN-2001	2001DE-01002337.	
QY	335	LysGlyThrValAlaPheHistYzAlaPheHisIleLeuPro	354		XX	XX	
Db	14441	AAGGGAACTGGTCTGTTCACTTTCGGGACAGGGTGTGCTATCTTCRCCCT 14500		PA	PA	(BADI) BASF PLANT SCI GMBH.	
QY	355	GlyValAlaLysProLeuAlaIlePheMetValAlaThrGluLeuValAlaGlyLeuLeu	374		XX	XX	Lerchl J, Renz A, Heinz E, Domerque F, Zaehringen U;

DR	WPI: 2002-644810/70. 2-PDSB; ABB98278, ABB98277, ABB98274.	Db	13841 AGGTGGAGCCGACTCCAGAGCTGCTGAAGATTCGGAGMATTGAGCTCTTTCCTG 13900
XX		Qy	155 ArgGluGlyLeuSerSerLysAlaTrpPheLeuIleGlnThrLeuIleAspAla 174
PT	Preparing ester containing polyunsaturated fatty acids, useful e.g. in animal or human nutrition, by transforming organism with desaturase gene from Phaeodactylum tricornutum.	Db	13901 AGGGAGCAACTTTCAAAGTTGCTAAATTGCTACGGAATGTT 13960
XX		Qy	175 AlaLeuPheAlaAlaSerIleAlaThrIleCystYsAspLysSerTyrTrpAlaIleVal 194
PS	Example 11; Page 154-170; 182pp; German.	Db	13961 GCTATTGTTGCTGGAGCATTTGCAAGACTATTTCAGGGTTTTG 14023
XX	The invention relates to preparing (M1) fatty acid esters (I) with an increased content of polyunsaturated fatty acids (II) with at least two double bonds by introducing into a (I)-producing organism a specific nucleic acid (A). (M1) is useful for preparing ester containing polyunsaturated fatty acids. Oils, lipids and (II) or their fractions, produced by (M1) are used in animal and human nutrition, cosmetics and pharmaceuticals, e.g. (II) are known to reduce levels of cholesterol in the blood and to protect against heart disease. Cells that express (A) are also used to identify (ant)agonists of desaturases, e.g. for modulating the yield and rate of production of particular fine chemicals in microorganisms (claimed). Also (A) and derived proteins can be used as markers of specific genomic regions and in evolutionary/protein structural studies. (M1) is suitable for large scale production (no known bioengineering method can produce (II) on a useful scale). The present sequence is that of the pUC19 based plant specific expression vector (ABV74273) expressing the Physcomitrella patens elongase (ABB98278); and the Phaeodactylum tricornutum desaturase (ABB98277 and ABB98274) of the invention. (updated on 07-AUG-2003 to correct OS field.)	Db	13991 LeuSerAlaSerIleLeuMetGlyLeuPheValGlnGlnCysGlyTriPheAlaHisAspPhe 214
CC		Db	14021 GCTTCAGCTTGATGATGGCTCTGTTCCAAACAGTGCGGAACTCCATGATT 14080
CC		Qy	215 LeuHisGlnGlnValPheGluAsnArgThralaAsnSerPhePheGlyTyrLeuPheGly 234
CC		Db	14081 CTCACAACTAGGTGTTGAGACAGCTGGCTTAATGAAGTTGGTATGATCGGC 14143
CC		Qy	235 AsnCysValLeuGlyPheSerValSerTrpTrpArgGlyLeuIleHisIleThr 254
CC		Db	14141 AACGCCGTTCTGGGGTTAGTAGCAGGGTGGTCAAGGAAACATACTCTCATCATGCT 14200
CC		Qy	255 AlaProAsnGluCysAspPheGluGlnTyrThrProLeuAspGluAspIleAspThrLeuPro 274
CC		Db	14201 GCTCCAATGAAATGCGATCAGACTAACCTACATGATAAGATATTGATGAAAGCTCCC 14260
CC		Qy	275 IleIleAlaTrpSerLysGluIleLeuValGluUserLysArgIleLeuIleArgVal 294
CC		Db	14261 CTACATTGCCTGGAGCAAGGACATACTGGCCACAGTTGAGAATAAGCACATTCTGGAAATC 14320
QQ	Sequence 17752 3P; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;	Qy	295 LeuGlnTyrGlnHistYrMetIleLeuProLeuAspLeuSerTrpThr 314
DB		Db	14321 CTCCAATACCAAGCATTCTGTTCTATGGGTCTGTGTTGGCT 14380
Qy		Qy	315 PheGlySerIleLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGlu 334
DB		Db	14381 TTGGGASCTGGAGATAACCTCTAACGGCTGACAGGTGTTGGAG 14440
Qy		Qy	335 LysGlyThrValAlaPheHistYrAlaTrpMetIleLeuProLeuSerTrpAlaAlaPheHisIleLeuPro 354
DB		Db	14441 AAGGGAACTGTTCTGTTCACTACTTTGGTCACTACTTCTCCCT 14500
Qy		Qy	355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeu 374
DB		Db	14501 GGT---TGGAAAGCCATTAGTATGGTACTGAGCTCATGTCGGCATCTGCTGCT 14557
Qy		Qy	375 GlyPheValPheThrLeuSerHisAspHistYrAsnGluUserLysAspPhe 394
DB		Db	14558 3GCTTTGTATTGGTACTAGCCACAATGGGATTTAGCTTAAAGAAATT 14617
Qy	1 MetAlaLeuValThrAspPheLeuGlyThrThr----TrpSerLys 17	Qy	395 ValArgAlaGlnValIleThrArgAsnThrLysArgGlyTyrTrpPheAspTrpPhe 414
DB	13385 ATGTCCTCTCTTCAGCGACTCTTCAGTTATGCTCTCAACTGTTGGTCA 13444	Db	14618 GGGAGTCACAGATCGTATCCACCGGGATATCAAGGAACATATACTCAACGACTGGTTC 14677
Qy	18 TyrSerValTyrThrHisSerTyraAlaGlyAsnTyrGlyProThrLeuIleGln 37	Qy	415 ThrGlyGlyLeuAspThrGlnIleGluIleHisLeuPheProThrMetProArgHisLys 434
DB	13445 CACAGTATAACAACCTTGAAG 13483	Db	14678 ACTGGTGGCCCTAAACAGGCCAAATAAGGCTCATCTTCTCCAAACAAATGCCAGGCTAAAT 14737
US-09-980-468-2 (1-483) × ABV74275 (1-17752)		Qy	416 GluAlaSerGlnValIleThrArgAsnThrLysArgGlyTyrTrpPheAspTrpPhe 414
Qy	1 MetAlaLeuValThrAspPheLeuGlyThrThr----TrpSerLys 17	Db	14738 TTAAACAAATAGCACCTAGCTGGGTGTTCTGTAAGAAACACGGCTCTGGTACGGAA 14797
DB	13484 CGTGTTCGGAAAGGGCTGCCGCTGCGGACTCGCAAGTCAGGCCACGAGGAAGGTCA 13543	Qy	417 AsnValSerValValGlyAlaSerValAlaLeuLysGluIleAlaAsp 474
Qy	38 LysValSer-----AlaGlnIleLysThrAlaGlyGlnThrLeuArgGlnArgSer 54	Db	14798 GACGTATCTATTGCTACGGCAACTGGTCAAGGTTTTGAAAGGAACTGGCG 14854
DB	13544 ACCCAGGGAACTGGGACTCGCAAGTCAGTCGAAAGCCACGAGGAAGGTCA 13603	Qy	418 TyrProLysTrpMetIleValLysGluLysValTyrAspIleLeuCysLysGluIleGlutYrAsp 454
Qy	55 ValGlnAspLysProGlyThrThrSerIleAlaAspValAlaSerHisAspArgPro 74	Db	14855 GAGGTATCTATTGCTACGGCAACTGGTCAAGGTTTTGAAAGGAACTGGCG 14878
DB	13604 TCTCAGTGGAAAG---TCGACACACCCCCTATCAGAAGTAGCCTACACAAGCCA 13660	Qy	419 GluAlaSerIleArgLeuHisAla 482
Qy	75 GlyAspCysTrpMetIleValLysGluLysValTyrAspIleSerArgPheAlaAspAsp 94	Db	14855 GAGGTATCTATTGCTACGGCAACTGGTCAAGGTTTTGAAAGGAACTGGCG 14878
DB	13661 AGGGATGCTGGATTGTTGTAAGAAACAAGGTGTTCCAAATTGTCGGACGAG 13720	Qy	420 HisProGlyGlyThrValIleSerThrThrPheGlyArgAspGlyThrAspValPheAla 114
Qy	95 HisProGlyGlyThrValIleSerThrThrPheGlyArgAspGlyThrAspValPheAla 114	Db	14855 GAGGTATCTATTGCTACGGCAACTGGTCAAGGTTTTGAAAGGAACTGGCG 14878
DB	13721 CATCCCCGGGGATCAGCTCTACATGGAAAATTCTCAAGACTTIAACAGCTTACATGGAAAGTGGAG 13780	Qy	421 ArgGluGluProProAlaAlaTrpLysGlnLeuAsnAspTyrGlyAspLeuAla 134
Qy	115 ThrPheHisProProAlaAlaTrpLysGlnLeuAsnAspTyrGlyAspLeuAla 134	Db	14855 GAGGTATCTATTGCTACGGCAACTGGTCAAGGTTTTGAAAGGAACTGGCG 14878
DB	13781 AGTGGTTCAGCTGCGGAGAGGCACTGGTACGTTCTACATGGAAAATTCTCAAGACTTIAACAGCTTACATGGAAAGTGGAG 13840	Qy	422 RESULT 11
Qy	135 ArgGluGluProLeuAspGluLeuLysAspTyrArgAspMetArgAlaGluPheVal 154	Db	14855 GAGGTATCTATTGCTACGGCAACTGGTCAAGGTTTTGAAAGGAACTGGCG 14878
ABQ76797			

ID ABQ76797 standard; DNA; 17752 BP.
 XX ABQ76797;
 AC ABQ76797;
 XX 25-MAR-2003 (First entry)
 XX DE BARA1 encoding delta6 elongase, delta6 and delta5 desaturase.
 XX KW Promoter; expression cassette; structural gene; plant; transgenic;
 KW linseed; fatty acid ester; polyunsaturated fatty acid; PUFAs; cosmetic;
 KW animal nutrition; human nutrition; pharmaceutical; cholesterol; blood;
 KW heart disease; seed-specific; ds.
 XX OS Physcomitrella patens.
 OS Phaeodactylum tricornutum.
 OS Synthetic.
 XX
 EH Key
 FT CDS Location/Qualifiers
 FT 11543 . .12415
 /tag= a
 /product= "delta6 elongase"
 /note= "from Physcomitrella patens"
 FT CDS
 FT 13313 . .14890
 /tag= b
 /product= "delta6 desaturase"
 /note= "from Physcomitrella patens"
 FT CDS
 FT 15791 . .17200
 /tag= c
 /product= "delta12 desaturase"
 /note= "from Phaeodactylum tricornutum"
 XX DE10102338-A1.
 PN DR 25-JUL-2002.
 XX 19-JAN-2001; 2001DE-01002338.
 XX PR 19-JAN-2001; 2001DE-01002338.
 PA (BADI) BASF PLANT SCI GMBH.
 XX PI Lerchl J, Duweling E, Bischoff F, Heinz E, Drexler H, Scheffler J;
 XX WPI; 2002-675961/73.
 DR P-PSDB; ABG73608, ABG73609, ABG73610.
 XX PT New expression cassette for plant genes, useful for preparing transgenic
 plants that have increased production of polyunsaturated fatty acids.
 XX PS Example 13; Page 158-174; 188pp; German.
 XX CC This invention describes novel expression cassette (EC) containing at
 least one each of plant promoter (P) and structural gene (SG) expressed
 in plants, flanked by specific restriction enzyme (RE) recognition sites.
 CC The EC has the structure (L1-P-SG-L2) n where L1 = is a polylinker
 (ABQ76798), L2 = any of three synthetic polylinker-terminator-polylinker
 sequences reproduced (ABQ76799-ABQ76801) or equivalent RE-site-containing
 sequences and n = 1-3. The invention discloses a vector containing this
 EC, an organism containing the EC or the vector and a transgenic plant
 containing a (non-)functional nucleic acid in the vector. Transgenic
 plants e.g. linseed can be prepared with improved production of fatty acid
 esters with an increased content of polyunsaturated fatty acids (PUFA),
 useful in animal and human nutrition, cosmetics and pharmaceuticals, e.g.
 CC PUFAs are known to reduce levels of cholesterol in the blood and to
 CC protect against heart disease. The expression cassettes of the invention
 CC provide increased and more efficient production of fine chemicals
 (especially PUFA), including seed-specific production. This sequence
 CC represents a nucleic acid sequence used to illustrate the method of the
 CC invention
 XX SQ Sequence 17752 BP; 4334 A; 4385 C; 4666 G; 4367 T; 0 U; 0 Other;
 SQ 14261 CTCATGCCCTGGAGCAAGACATACTGGCCACAGTGAAGAAATTGCGAATC 14320

Alignment Scores:

producing plant oils with increased content of unsaturated fatty acids.

XX PT Example 6; Page 51; 69pp; German.

XX XX

XX This invention describes a novel isolated nucleic acid (I) encoding polypeptides (II) with Delta6-acetylenase and/or Delta6-desaturase activity. The invention also describes (a) amino acid sequences encoded by (I); (b) an expression cassette (EC) containing (I) linked to one or more regulatory sequences; (c) a vector containing (I) and EC; (d) organisms containing (I), EC or the vectors of (c); (e) preparation of (A) by introducing (I) or EC into an oil-producing organism; (f) proteins (IIa) of 172 aa or 178 aa (given in the specification); (g) production of (A) or TG by using (Ia); and (h) (A) and TG produced by method (g). (I) are used to produce transgenic plants (or other organisms) that produce oils or triglycerides (TG) with increased content of unsaturated fatty acids (A) and to isolate related sequences by homology screening. (A), or TG containing them, are useful in human nutrition (e.g. infant foods), animal feeds, pharmaceuticals and cosmetics. Derivatives of (I), e.g. antisense sequences or ribozymes, can be used to suppress expression of (II), resulting in oils with increased content of saturated fatty acids.

XX XX

XX Sequence 520 BP; 124 A; 116 C; 136 G; 144 T; 3 U; 0 Other;

XX XX

XX Alignment Scores:

XX Pred. No.: 2.97e-95 Length: 520

XX Score: 925.00 Matches: 172

XX Percent Similarity: 100.00% Conservative: 1

XX Best Local Similarity: 99.42% Mismatches: 0

XX Query Match: 35.65% Indels: 0

XX DB: 4 Gaps: 0

XX US-09-980-468-2 (1-483) x AAF25731 {1-520}

XX QY 251 IleHisHisthrAlaProAsnGluCysAspGlnTyrThrProLeuAspGluAspIle 270

XX DB 2 ATTCACTCATACTGCTCCGAAATGAGTCGCAACGAACTAACACGGTCTG3TTACGAACTGACATT 61

XX QY 271 AspThrLeuProIleAlaTrpSerIlysGluIleLeuAlaThrValGluSerIlysArg 290

XX DB 62 GATACTCTCCCCTCATGCTGGAGAAATTGGCCACCGTGTGAGGAAAGAGAAAGAGAAAGAGA 121

XX QY 291 IleLeuArgValLeuGlnHistyrMetIleLeuProLeuIlePheMetAlaArg 310

XX DB 122 ATTTGGGAATGGCTCGATATCGACTACATGATCTGCCTCTATGTTCATGCCCG 181

XX QY 311 TyrSerTrpThrPheGlySerLeuLeuSerIlysGlnProAspLeuSerThrThrLys 330

XX DB 182 TACAGTTGGACTTTGGAAAGTTGGCTCTCACATTCAATCTGATTGAGCACGACAAG 241

XX QY 331 GlyLeuIleGluLysGlyThrValAlaPheHistyrAlaTrpPheSerTrpAlaAlaPhe 350

XX DB 242 GGATTGATAAGAAGGAAACAGTTGCTTCACTAGCCCTGGATCTGAGCTGCTGGTCC 301

XX QY 351 HisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla 370

XX DB 302 CATATTTGGGGTCTGGCTAACGCTTCTGGATCTGAGCTGCTGGTCAATGAA 361

XX QY 371 GlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGlu 390

XX DB 362 GGTTTGGTTGGGATTCTGGTGTAGTTGCTGTTAGTTGAGTCACATGGAAAGGAGTTACAATGAA 421

XX QY 391 SerLysAspPheValArgAlaGlnValIleThrArgAsrThrLysArgGlyTrpPhe 410

XX DB 422 TCGAAGGACTTCGTGAGAGCCCCAGGTATTACCAACCCGTAAACCAAGGAGCCAGATGAG 481

XX QY 411 AsnAspTTPheThrGlyGlyLeuAspPheThrGlnIleGlu 423

XX DB 4B2 AACGATTGGTTCACTGGGGACTCGACACCCAGATGAG 520

XX RESULT 12

XX AAF25731

XX DT 06-APR-2001 (first entry)

XX ID AAF25731 standard; DNA; 520 BP.

XX XX

XX DE C. Purpureus delta6-acetylenase/delta6-desaturase DNA SEQ ID NO 5.

XX KW Delta6-acetylenase; delta6-desaturase; unsaturated fatty acid;

XX transgenic plant; plant oil; triglyceride; nutrition; animal feed;

XX cosmetic; ds.

XX OS Ceratodon purpureus.

XX PN WO200075341-A1.

XX PD 14-DEC-2000.

XX PP 07-JUN-2000; 2000WO-EP005274.

XX PR 07-JUN-1999; 99DE-01025718.

XX PR 22-DEC-1999; 99DE-01062409.

XX PA (BADI) BASF AG.

XX PI Heinz E, Stymne S, Lee M, Girke T, Sperling P, Zaehringer U;

XX WPI; 2001-112150/-2.

DR P-PSDB; AAB46437.

XX Nucleic acid encoding delta6-acetylenase or desaturase, useful for

XX PT RESULT 13

XX AAZ47129

Db 1261 AAAAGTACAATGTCGATAACCACCCGTATGATCGAGGGAACTGCAAGGGCTTT 73
 QY 467 LYSALalenuLysGluileAlaAspGluAlaSer 477
 Db 1321 AGCGGTCGAACGAGGTCTCCAAGGCTGCCTCC 1353

RESULT 14

AAF25234 standard; DNA; 1374 BP.
 XX AAF25234;
 AC XX 301-APR-2001 (first entry)
 DE Nucleotide sequence of a fungal delta6 desaturase.
 XX KW delta6 desaturase; desaturase gene; elongase gene; fatty acid;
 KW eicosanoid; nutrition; infant formula; dietary supplement;
 KW dietary substitute; animal feed; ss.
 XX Mortierella alpina.

FH Key
 CDS Location/Qualifiers
 FT 1. -1374 /*tag= a
 FT /product= "delta6 desaturase"
 XX PN WO2001034636-A1.
 XX PD 18-JAN-2001.
 XX PF 11-JUL-2000; 2000WO-US019011.
 XX PR 12-JUL-1999; 99US-00351525.
 XX PA (JYOH-) UNIV OHIO.
 PI Kopchick JU, Kelder B;
 XX DR 2001-192622/18.
 DR P-PSDB; AAB31684.
 XX PT New compositions comprising cells that express desaturases and elongases,
 PT for synthesizing essential fatty acids or long-chair polyunsaturated
 PT fatty acids, used in nutritional, cosmetic or animal feed formulations.
 XX Disclosure; Fig 8; 93pp; English.
 XX The present sequence encodes a delta6 desaturase. The desaturase
 CC polynucleotide sequence was used to transfet mammalian cells, to produce
 CC animal cells expressing a desaturase gene and/or an elongase gene.
 CC Compositions comprising cells of the invention are useful for
 CC synthesising essential fatty acids, their derivatives or downstream
 CC products, as well as altered levels of long-chain polyunsaturated fatty
 CC acids and eicosanoids. The compositions are useful in nutritional
 CC formulae, e.g. infant formula, dietary supplements or dietary substitutes
 CC for both humans and animals. The compositions are also useful in cosmetic
 CC or animal feed formulations. Furthermore, the compositions may also be
 CC used as fat free media or as research reagents
 XX Sequence 1374 BP; 257 A; 386 C; 378 G; 353 T; 0 U; 0 Other;

SQ Alignment Scores:
 Pred. No.: 4.01e-85 Length: 1374
 Score: 941.50 Matches: 177
 Percent Similarity: 55.21% Conservative: 72
 Best Local Similarity: 39.25% Mismatches: 159
 Query Match: 32.43% Indels: 43
 DB: 5 Gaps: 10

Db 62 ThryrSerLeuAlaAspVal-----AlaSerHisAspArg 73
 Db 25 ACGTTACTGGGCCGAGGTTTGAATGCCGAGGCTCTGAATGAGGGCAAGAAGGGATGCC 84
 QY 74 ProGlyAspCystrpMetIlevallysValtyraspIleSerArgPheAlaAsp 93
 Db 85 GAGGCACCCCTCTTGATGATCATGACAACAGGTGTACGATGTTGGAGACTGAGTCCT 144
 QY 94 AspHisProGlyGlythrvallieserThrTyrPheGlyArgaspGlyThrAspValPhe 123
 ID 145 GATCATCCCCTGGTGAAGTGGCAAGGACGGACTGAGTCCT 204
 QY 114 AlaThrPheHisProProAlaAlaTriPheGlyLeuLeuLysAspTyrrArgaspMetArg 150
 Db 205 GACACTTTACCCCGAGGCTGCTGGAGACTCTGGCAACTTTACGTTGGTGATATT 264
 QY 134 -----AlaArgGluGluProLeuAspGluLeuLeuLysAspTyrrArgaspMetArg 150
 QY 265 GACGAGAGCCGACCGCGATATAAGAAATGACTTGGCCGAGGGTCCGAAAGCTGCGT 324
 QY 151 AlaGluPheValArgGluGlyLeuPheLySSerLysAlaTrpPheLeuLeuGlnThr 170
 Db 325 ACCRTGTTCACTTCAGTCAGTCAGTCTGGTACTACGATTCTCAAGGCATACTACGCTTCAAGGTC 384
 QY 171 LeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIleCysTyr-----AspLys 188
 Db 385 TCGTTCAACTCTGCACTCTGGGTTGTCAGCGTCACTGTGGCAAGGCCAGAAC 444
 QY 189 SerTyrrTrpAlaIleLeuSerAlaSerIleLeuMetGlyLeuPheValGlnGlnCysGly 208
 Db 445 TCGACCCCTGCCAACGTTGCTCCTGGCTGCACCTTCTGGCTGCTGGCTGCGGGAA 504
 QY 209 TrpLeuAlaHisAspPheLeuHisGlnGlnValPheGluAspArgThrAlaAsnSerPhe 228
 Db 505 TGGTGGACTCACGACTTTTGCAATCACAGGTCTTCCAGGACGGTGTCTCGTGGTGAAGGACAAAG 624
 QY 229 PheGlyTyrePheGlyAsnCysValLeuGlyPheSerValSerTrpTrpArgThrLys 246
 Db 565 TTGGGGGCCCTCTGGAGGTGTCTGGTGGTGGTGAAGGACAAAG 624
 QY 249 HisAsnIleHisIsthrAlaProAsnGluCysAspGluGlnTyrThrProLeuAspGlu 268
 Db 625 CRCAAACACTACCACGCCACCCCTCTGTTGACCTGGAGTGTCTGGTGGAGATGTCTGGAT 729
 QY 286 ValGluSerIlysArgIleLeuArgValLeuGlnHistYrGlnHistYrMetIleLeu----- 303
 Db 730 GTCCCCAGATGAGGAGCTGACCCGCTGATG-----TGGTCCGGGTTCATGGTCCCTGAAACAG 783
 QY 304 -----ProLeuLeuPheMetAlaArgTyrSerTrpTrpPheGlySerLeu 318
 Db 784 ACCRTGTTACTCCCATCTCGTTGCTGTTGAGCATGCGTTGGAGTGTCTGGTCCAGTCCATT 843
 QY 319 LeuPheThrPheAsnProAspLeuSerThrThrLys----- 330
 Db 844 CTCTTGTGCTGTC-----CCTAACGGTAGGCCACAGCCCTGGCCGCTCTCTGGCTCCAGTCCATT 903
 QY 331 GlyLeuIleGluLysGlyThrvAlaPheHistYrAlaTrpPheSerTrpAlaAlaPhe 350
 Db 901 TCGTTGGCTGAGCAGCTGGCTGCTGGATGCACTGGACCTGGTACCTGGCCACCATGTC 960
 QY 351 HisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla 370
 Db 961 CTGTTTCACTCAAGGATCCCGTCAAACATGCTGGGTACTTTRGGT3TCGTCAGGGCTGTGC 1020
 QY 371 GlyLeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyAsnGlu 390
 DB: 1021 GAAAACCTTGTGGCATGGTGTCTCGCTCAACCACAAACGGTATGCTGTGATCTCGAAG 1080
 QY 391 SerLys-----AspPheValArgAlaGlrValIleThrThrArgAsnThrLys 406

enzyme can be used to produce polyunsaturated fatty acids, which can be used for treating malnutrition, in pharmaceutical compositions, in cosmetics or in animal feed. The polyunsaturated fatty acids can be used for treating e.g. restenosis after angioplasty, inflammation, rheumatoid arthritis, asthma, psoriasis, cancer, diabetes or eczema or reduce blood pressure. They can also be used to inhibit platelet aggregation, cause vasodilation, lower cholesterol levels, inhibit proliferation of vessel wall smooth muscle and fibrous tissue, reduce or prevent gastrointestinal bleeding and other side effects caused by non-steroidal anti-inflammatory drugs, prevent or treat endometriosis and premenstrual syndrome, treat myalgic encephalomyelitis and chronic fatigue after viral infections, treat AIDS, multiple sclerosis, acute respiratory syndrome, hypertension and inflammatory skin disorders.

XX 1261 AAAAGTACAATGTCGGATAACACCACCGGTATGATCGAGGGACTGGAGGTCTTT 1320

QY 467 LysAlaLeuLysGluIleAlaAspGluAlaSer 477

Db 1321 A3CCGTCTGAACGAGGTCTCCAAGGCTGCCTC 1353

RESULT 15

AAV63624 standard; cDNA: 1617 BP.

ID AAV63624

XX AAV63624;

AC XX

DT 15-FEB-1999 {First entry}

XX DE encoding a delta-6 desaturase enzyme.

XX DE delta-6 desaturase; polyunsaturated fatty acid; malnutrition; KW inflammation; rheumatoid arthritis; asthma; cancer; diabetes; eczema; platelet aggregation; vasodilation; cholesterol level; endometriosis; premenstrual syndrome; myalgic encephalomyelitis; chronic fatigue; AIDS; multiple sclerosis; acute respiratory syndrome; hypertension; inflammatory skin disorder; ss.

XX OS Mortierella alpina.

XX FR Location/Qualifiers

FT 71. -1444

FT /*tag= a

FT /product= "delta-6 desaturase"

XX PN WO9846763-A1.

XX PR 11-APR-1997; 97US-00834655.

XX PD 22-OCT-1998.

XX PP 10-APR-1998; 98WO-US007126.

XX PR 1998-594582/50.

PI Knutzon J, Mukerji P, Huang Y, Thurmond J, Chaudhary S;

PI Leonard AE;

XX DR P-PSDB; AAW84137.

XX PT New isolated fatty acid desaturase enzymes - used for the production of polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, nutritional compositions, cosmetics or animal feed.

XX PT Polyunsaturated fatty acids for use in, e.g. pharmaceutical compositions, invention. The enzyme sequence is used in the methods of the invention. The specification describes methods for desaturating a fatty acid and for producing a desaturated fatty acid by expressing increased levels of a desaturase. The present desaturase is an enzyme which introduces a double bond carbons 6 and 7 from the carboxyl end of a fatty acid molecule. The enzyme can be used for desaturating fatty acids. The

QY 407 ArgGlyTrpPheAsnAspTrpPheThrGlyLeuAspPheThrGlyIleGluIleSle 426

Db 1141 CCGGGTCTTGTCAAACGGTCACTATGATCGAGACCTTG 1200

QY 427 PheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluIleLeuCys 446

Db 1201 TTCCCTTGATGCCAACACTTCAAGATCCAGCTGTGTCAGACCCCTGTGC 1260

QY 447 LysLysHisGlyLeuGlutYraspAsnValSerValAlaValVal 466

Db Sequence 1617 BP; 310 A; 470 C; 410 G; 427 T; 0 U; 0 Other;

QY 1617 Length: 1617

Db 841.50 Matches: 177

Score: 55.21% Conservative: 72

Percent Similarity: 39.25% Mismatches: 159

Best Local Similarity: 3.2-43% Indels: 43

Query Match: 2 Gaps: 13

DB: US-C9-980-468-2 (1-483) x AAV63624 (1-1617)

QY 62 ThrTyrSerLeuAlaAspVal-----AlaSerHisAspArg 73

Db 95 ACGGTTACTGGGCCAGGTTTGAATGCCAGGGCTCTGAATGAGGGCAAGAAGGATGCC 154

QY 74 ProGlyAspCystripMetIleValLysGluLysValTyrAspIleSerArgPheAlaAsp 93

Db 155 GAGGCACCCCTCTGATGATCATCGACAACAAAGGTGTACGAT3TCCCGGA3TTGTCCT 214

QY 94 AspHisProGlyGlyLysValIleSerThrTyrPheGlyIgYAspGlyThrAspValPhe 113

Db 215 GATCAGCCGGTGGAAAGTGTGATTCTCACGACGTTCAAGGACGGACTGAAGTCRTT 274

QY 114 AlaThrPheHisProProAlaAlaAspLysGlnIleAsnAspTyrTyrIleGlyAspLeu 133

Db 275 GACACITITACCCCCGAGGCTGCTTGGGAGACTCTTGCACACTTTACGTTGGTATATT 334

QY 134 -----AlaArgGluGluProLeuAspGluIleLeuLysAspTyrIargAspMetArg 150

Db 335 GACGAGAGGCAACCGGCAATGATGACTTTGGGAGCTTGGCTGGCTGCGT 394

QY 151 AlaGluIlePheValArgGluIleLeuPheLysSerSerLysAlaTrpPheLeuGlnThr 170

Db 395 ACCTTGTTCAGTCTCTGGTTACTACGATTCTCAAGGCATACTACGCTCTCAAGGTC 454

QY 171 LeuIleAsnAlaAlaLeuPheAlaAlaSerIleAlaThrIleCystYr-----AspLys 188

Db 455 TCGTTCAACCTCTGCATCTGGGGTTCAGTCTCTGGTTACTACGATTCTCAAGGTC 514

QY 189 SerTyrTrpAlaIleLeuSerAlaSerIleMetGlyLeuPheValGlnCysGly 208

Db 515 TCGACCCCTGCCAACGGCTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 574

QY 209 TrpLeuAlaHisAspPheLeuHisGlnGlnValPheGluAsnArgThrAlaAsnSerPhe 228

Db 575 TGGTTGGCTCAGCACTTTCGATCTCCAGGACCGTTCTGGCTGGCTGGCTGGCTGG 634

QY 229 PheGlyTyrLeuPheGlyAsnCysValLeuGlyPheSerValSerTrpIleArgThrLys 248

Db 635 TCGGGGCCCTCTGGAGGTGTCTGCCAGGGCTCTGGCTGGCTGGCTGGCTGG 694

QY 249 HisAsnIleHisthralaProAsnGluCysAspGluGlnTyrThrProLeuAspGlu 268

Db 695 CACAAACACTCACCACGCCAACGTCACGGCAG-----GATCCC 739

QY 269 AspIleAspThrLeuProIleAlaTrpSerLys-----GluIleLeuAlaThr 285

Db 740 GACATTGACACCCACCTCTGGCTGGAGTGGCTGGCTGGCTGGCTGGCTGGCTGG 799

Qy 286 ValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyrMetIleLeu----- 303
 Db 800 ||| :::: | | :||| :||| :||| :||| :||| :||| :||| :||| :|||
 GTCAGATGGAGCTGACCCCGCATG-----TEGTGGCCTTCATGGTCCTGAAACCAG 853

Qy 304 -----ProLeuLeuPheMetAlaArgIlysSerTrpThrPheGlySerLeu 318
 Db 854 ACCTGGTTTTACTTCCCATTCTCTCGTTCGCCGTCCTCCTGGCCTCCAGTCAT 913

Qy 319 LeuPheThrPheAsnProAspLeuSerThrThrLys----- 330
 Db 914 CTCTTGTGCTG---CCTAACSGTCAG3CCCACAGCCCTCGGCGCGTGTGCCCATC 970

Qy 331 GlyLeuIleGluLysGlyThrValAlaPheHistYralaTrpPheSerTrpAlaAlaPhe 350
 Db 971 TCGTTGGTCGAGCTGCTCGCTTGCGATGCACTGGAACTGGTACCTGCCTGCACCATGTTTC 1030

Qy 351 HisIleLeuProGlyValAlaIlysProLeuAlaTrpMetValAlaThrS1LeuValAla 370
 Db 1031 CTGTTCATCAAGGATCCCGTCAACATGCTGGTGTACTTTTGTTGGCTGCGGGTGTGC 1090

Qy 371 GlyLeuLeuIleGlyPheValPheThrIeuSerHisAsnGlyLysGluValItyrAsnGlu 390
 Db 1091 GGAAACTTGTGGCGATCGTGTCTCGCTRAACCACACGGTATGCCTGTGATCTCGAAG 1150

Qy 391 SerLys-----AspPheValArgAlaGlnValIleThrThrArgAsnThrLys 406
 Db 1151 GAGGAGCCGCTCGATATGGATTCTTCACGAAGCAGTCATCACGGCTGTGATGTCCAC 1210

Qy 407 ArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisIleu 426
 Db 1211 CGGGCTCATTTGCCAACCTGGTCACTGGTCACTGGGATGGATTGAACTATCAGATCGACCACITG 1270

Qy 427 PheProThrMetProArgHisAsnNtysPrlySileAlaProGlnValGluAlaLeuCys 446
 Db 1271 TTCCCTTTCGATGGCTGCCACAACTTTCAAAGATCCGCTGTCGAGACCCCTGTGC 1330

Qy 447 LysLysHisGlyLeuGluItyrAspAsnValSerValAlaValAlaValVal 466
 Db 1331 AAAAAGTACAATGTCGATACCAACACCGSTATGATGAGTCAGAGGTCTTT 1390

Qy 467 LysAlaLeuLysGluIleAlaAspGluAlaSer 477
 Db 1391 AGCGTCTGAAACGAGTCTCCAGGCTGGCTCC 1423

Search completed: June 19, 2004, 03:06:48
 Job time : 689 secs

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OM protein - protein search, using sw model

Run on: June 16, 2004, 19:00:51 ; Search time 18 Seconds
 (without alignments)
 1397.216 Million cell updates/sec

Title: US-09-980-468-2
 Perfect score: 2595
 Sequence: 1 MALVTDLNFGLTWSKYV.....AVVKALLEIADEASIRLHAE 483

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 3.5

Searched: 141681 seqs, 52070155 residues
 Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries
 Database : SwissProt_42;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	500.5	19.3	444	1	FADS_BRAVE	Q9DEX7;	09dex7 brachydanio
2	200	7.7	359	1	LLCD_SYNYY3	Q08871	synechocyst
3	193.5	7.5	132	1	CYB5_BORCF	Q04354	borage offi
4	190.5	7.3	137	1	CYB5_ORYSA	P49100	oryza sativ
5	179.5	6.9	136	1	CYB5_TOBAC	P49098	nicotiana t
6	172.5	6.6	135	1	CYB5_CUSRE	P49097	cuscuta ref
7	172	6.6	135	1	CYB5_TOBAC	P49099	nicotiana t
8	170.5	6.6	134	1	CYB5_ARATH	Q4B845	arabidopsis
9	166.5	6.4	900	1	NIA2_LOTUA	P39980	lotus japon
10	164	6.3	918	1	NIA2_CUCMA	P17569	cucurbita m
11	162.5	6.3	435	1	FD3D_ARATH	P4B622	arabidopsis
12	160.5	6.2	864	1	NIA2_VOLCA	P236841	volvox cart
13	160	6.2	120	1	CYB5 YEAST	P40312	saccharomy
14	160	6.2	890	1	NIA2_PHAU	P239866	phaseolus v
15	159.5	6.1	380	1	FD3E_RICCO	P322291	phaseolus a
16	158.5	6.1	460	1	CY51_SCHPO	P48619	ricinus com
17	157	6.1	124	1	NIA2_SOYBN	P044391	schizosacch
18	157	6.1	890	1	NIA2_SOYBN	P399870	glycine max
19	154.5	6.0	318	1	NIA2_CHLVU	P011170	chlorella v
20	154	5.9	414	1	CYB5_DROME	P19967	drosophila
21	154	5.9	591	1	CYB2 YEAST	P00175	saccharomy
22	154	5.9	886	1	NIA1_SOYBN	P54233	glycine max
23	153.5	5.9	134	1	CY51_ARATH	Q42342	arabidopsis
24	153	5.9	917	1	NIA1_ARATH	P11832	arabidopsis
25	153	5.9	917	1	NIA2_ARATH	P11035	arabidopsis
26	150	5.8	134	1	CYB5 BRAOL	P40934	brassica ol
27	150	5.8	911	1	NIA1_BRANA	P39867	brassica na
28	149	5.7	881	1	NIA1_PHAU	P39865	phaseolus v
29	149	5.7	904	1	NIA2_TOBAC	P08509	nicotiana t
30	149	5.7	911	1	NIA2_BRANA	P39868	brassica na
31	148.5	5.7	146	1	CYMS RAT	P04166	rattus norv
32	148.5	5.7	453	1	FD3C SOYBN	P48621	glycine max
33	148	5.7	384	1	SCST YEAST	Q03529	saccharomy

3.4 147.5 5.7 902 1 NIA PHYIN
 3.5 147 5.7 131 1 CYB5 RHIST
 3.6 146.5 5.6 380 1 FD3E SOYBN
 3.7 146.5 5.6 386 1 FD3E ARATH
 3.8 143.5 5.5 926 1 NIA SPICL
 3.9 143 5.5 443 1 FD6C BRANA
 4.0 142 5.5 129 1 CY52 SCHPO
 4.1 142 5.5 911 1 NIA LYCES
 4.2 141.5 5.5 379 1 FD3E TOBAC
 4.3 141 5.4 383 1 FD62 SOYBN
 4.4 141 5.4 898 1 NIA BETVE
 4.5 141 5.4 909 1 NIA PETHY

ALIGNMENTS

RESULT 1

FADS_BRAVE STANDARD PRT; 444 AA.

AC Q9DEX7;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DB Delta-5/delta-6 fatty acid desaturase (EC 1.14.19.-).

GN FADS2 OR FADSD6.

OS Brachydanio rerio (zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

NCBI TaxID:7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX Hastings N., Agaba M., Tocher D.R., Leaver M.J., Dick J.R., Sargent J.R., Teale A.J.;

RT "A vertebrate fatty acid desaturase with delta5 and delta6 activities.";

RJ Proc. Natl. Acad. Sci. U.S.A. 98:14304-14309(2001).

CC !- FUNCTION: Fatty acid desaturase with both delta-5 and delta-6 activities. May represent a component of the polyunsaturated fatty acid biosynthesis pathway.

CC !- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC !- SIMILARITY: Belongs to the fatty acid desaturase family.

CC !- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.

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CC EMBL; AF309556; AAG25710.1; .

DR HSSP; P00173; 1JEX.

DR ZFIN; ZDB-GENE-011212-1; fads2.

DR InterPro; IPR001199; Cyt B5.

DR InterPro; IPR005804; FA_desat_fam.

DR Pfam; PP00487; FA_desaturase_1.

DR Pfam; PF00173; heme1; 1.

DR PRINTS; ER00363; CYTOCHROMEB5.

DR ProdDom; PDD000612; Cyt B5; 1.

DR InterPro; PDD01081; FA_desat_fam; 2.

DR PROSITE; PS00191; CYTOCHROME_B5_1; FALSE_NEG.

DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

DR Fatty acid biosynthesis; Oxidoreductase; Heme.

DR DOMAIN 18 95 HEME-BINDING.

FT METAL 53 53 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT METAL 76 76 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

SQ SEQUENCE 444 AA; 52032 MW; 62A25AIDC1DC0F65 CRC64;

Query Match Score 500.5; DB 1; Length 444;
 Best Local Similarity 28.8%; Pred. No. 1.5e-34;
 Matches 130; Conservative 78; Mismatches 164; Indels 79; Gaps 16;

Qy 62 TYSLADVA~~SHDRPGDCWMIVK~~EYDISRFADDHPGG-TWISTYGRDGTDFATFHP- 118
 Db 20 SYT~~WEVQKHTKHG~~DQWVVVERKVINSQWV~~KRHPGGLRILGH~~YAGEDATEAFTAFHPNL 79

Qy 119 PAAWKQ~~LNDYYIGDILAREEPLDE~~-LLKDYRD~~MRAEF~~YREGFLFKSSKAWFLLQTLI 172
 Db 80 QLVRKYL~~KPLLISELEAS~~EPSQDRQ~~NAALVED~~FRALRERLEAEGC~~EKT~~QP~~FFF~~FA~~LH~~GH 139

Qy 173 KHALFAA~~SAT~~IC~~YDKSYWA~~-IVL~~SASIM~~MLFVQ~~QCCM~~LAHC~~FIE~~Q~~Y~~VENTRANSFFGY 232
 Db 140 ILL~~EAIAFM~~MWTFG~~TG~~WNTLIVAVILATAQS~~QAGWL~~QHDFG~~EL~~SVEK~~TSGMNHL~~VHK 199

Qy 232 LFGNCV~~GFSVSWRTKHN~~IHTAPNECD~~EQYT~~PLDEDID~~ITLPI~~AWSKE~~LLATE~~--- 287
 Db 200 FVIGHLK~~GASAGWNHR~~FQHHAKP~~NIFKK~~--DPDV~~NML~~---NAFV~~VGNVQ~~P~~VEX~~ 249

Qy 288 SKRILRV~~QYQH~~YMLP~~LMARYS~~WT~~FGSLL~~FTNPD~~STKGL~~IEKGT~~VA~~FHYA~~WPSW~~ 347
 Db 250 GVKK~~KHLPYNH~~-----QH~~KY~~-----Q~~Y~~-----V~~YFQF~~ 281

Qy 348 AAFH--ILPGVAKPL~~AMVA~~-----TELV---AGLLLG~~F~~-----VFTL~~S~~ 381
 Db 282 QIFHN~~MISHGMWVDL~~LCISYYVRYFLCYTOFYGV~~WAIL~~LFNFV~~REME~~SHFW~~WWTQMS~~ 341

Qy 382 HNGKEV-YNESK~~OFFVRA~~QV~~ITTRNT~~KRGW~~FND~~WT~~GGLDTQ~~I~~EHL~~FPTM~~PRHENY~~PKIAP 440
 Db 342 HCPMNIDYEKNQDWLSMQLWATCNIEQSA~~ND~~WES~~QH~~INFQ~~EHL~~FPTV~~PRHENY~~WRAAP 401

Qy 441 Q~~VEALCKRHGLE~~YDNVSVVGASV~~AVVKALKE~~ 471
 Db 462 RURALCEKYG~~VKX~~Q~~EKTLYGA~~FADI~~IRSLEK~~ 432

RESULT 2
 LLCD_SYN₃
 ID LLCD_SYN₃ STANDARD: PRT; 359 AA.
 AC Q08871;
 DP 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Linoleoyl-CoA desaturase (EC 1.14.19.3) (Delta(6)-desaturase).
 GN DE56 OR SLL0262.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyano~~bacteria~~; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirosewa M., Sugiura M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Isolation of a delta 6-desaturase gene from the cyanobacterium
 Synechocystis sp. strain PCC 6803 by gain-of-function expression in
 Anabaena sp. strain PCC 7120.";
 RL Plant Mol. Biol. 22:293-300 (1993);
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268723; PubMed=9108131;
 RA Sayanova O., Smith M.A., Lapinskas P.A., Stobart K., Dobson G.,
 RA Christie W.W., Shewry P.R., Napier J.A.;
 RT "Expression of a borago desaturase cDNA containing an N-terminal
 cytochrome b5 domain results in the accumulation of high levels of
 delta6-desaturated fatty acids in transgenic tobacco.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4211-4216 (1997).
 CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
 carrier for several membrane bound oxygenases (By similarity).
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane. Bound to the
 CC -!- cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b5 family.
 CC -!- COFACTOR: Iron.

Query Match Score 200; DB 1; Length 359;
 Best Local Similarity 24.0%; Pred. No. 2.6e-09;
 Matches 86; Conservative 50; Mismatches 141; Indels 82; Gaps 17;

Qy 151 AEFVREGLEKSSKAWFLLQ~~TLINAA~~-LFAASIA~~TIC~~YDKSYWA~~AI~~V~~LSA~~-----SLMGLF 203
 Db 25 AFYFREG~~HLT~~Q~~RD~~DNP~~SMYL~~K~~T~~L~~II~~W~~ML~~LSA~~SA~~-----WAFVLF~~APV~~V~~P~~VRLLG~~C~~M 73

Qy 204 VQQCGW~~LA~~-----HDFLHQ~~QVF~~ENRT~~AN~~S~~F~~G~~V~~SV~~S~~WR~~T~~KHN-~~I~~HHTAP 256
 Db 74 VIALAL~~ARAF~~FSFN~~VGD~~ANHAYSSNPHIN~~VLGM~~TYD-FVGLSSFLW~~YRHN~~LHHTYT 231

Qy 257 NEC~~DEQY~~TP~~LD~~DT~~PL~~DEDID~~TL~~PI~~LA~~WS~~K~~EL~~LA~~TE~~S~~KR~~IL~~RV~~YQH~~YMLP~~LMARYS~~WT~~FG~~ 316
 Db 132 N-----ILGH~~D~~VE-----HGDDGAVR~~MS~~PEQ~~EHV~~-GIYRFQ~~QFYI~~W~~GLY~~L~~IP~~PFYW-- 176

Qy 317 SLLFTFNPD~~LS~~TTKG-----LIEKGT~~WAFHYA~~W~~FSWA~~-AFHILP~~GVAKP~~--LA 361
 Db 177 --FLYDV~~V~~L~~V~~N~~K~~YHD~~H~~K1P~~F~~Q~~P~~PLE~~A~~LSL~~L~~GI~~L~~W~~LG~~Y~~V~~FG~~L~~PL~~A~~GF~~S~~SI~~P~~E~~V~~L~~I~~ 233

Qy 362 W~~IVVATEL~~V~~AGL~~LLG~~FVFTL~~SHNGKEV~~T~~YNE~~SKDF~~V~~R~~-----AQVIT~~TRN~~--T 405
 Db 234 GAS~~VTYMT~~Y~~GI~~w~~YCT~~MLAH-----V~~LESTEFL~~PD~~G~~E~~S~~GA~~ID~~Q~~IR~~T~~TAN~~F~~AT~~ 288

RESULT 3
 CYB5_BOROF
 ID CYB5_BOROF STANDARD: PRT; 132 AA.
 AC 004354;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

Qy 406 KRGW~~END~~W~~F~~T~~G~~GLDTQ~~I~~E~~H~~L~~F~~PTMP~~H~~Y~~N~~PKIA~~P~~Q~~V~~EA~~L~~CKKH~~GLEY~~D~~N~~V~~S~~V~~G~~A~~S~~V~~A~~ 464
 Db 289 NNPPWN-W~~E~~CG~~GLN~~NH~~H~~Q~~T~~TH~~H~~L~~F~~P~~N~~TC~~I~~H~~Y~~Q~~L~~EN~~I~~IK~~D~~V~~C~~Q~~E~~F~~G~~Y~~E~~X~~K~~Y~~P~~T~~F~~K~~A~~A~~I~~A 345

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CC EMBL; X75670; CAA53366.1; -. DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 CC PIR; S46307; S46307. DR HSSP; P00171; 1EHB.
 CC Gramene; P49100; -. DR InterPro; IPR001199; Cyt_B5.
 CC Pfam; PF00173; heme_1; 1. DR PF00173; heme_1; 1.
 CC PRINTS; PR0363; CYTOCHROMEB5. DR ProdCom; PD000612; Cyt_B5; 1.
 CC DR PROSITE; PS00255; CYTOCHROME B5_2; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome.
 KW FT TRANSMEM 108 128 POTENTIAL.
 DR PRODOM; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome.
 FT TRANSMEM 104 124 POTENTIAL.
 FT METAL 37 37 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 61 61 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 132 AA; 14556 MW; 96EF72A06F2E8C5B CRC64;
 Query Match 7.5%; Score 193.5; DB 1; Length 132;
 Best Local Similarity 33.8%; Pred. No. 2.6e-09;
 Matches 48; Conservative 24; Mismatches 39; Indels 31; Gaps 6;
 Qy 54 YSLADVASHDRPGDCWMIVKEKVKYDISRFAADDHPGG-TVISTYFGRDGTDV 112
 DB 2 SNDNKK--VYTLEEVAKHNSKDKCWLIGGKVYNVSKFILEDHPGGDDVLLSSTGKDADDD 59
 Qy 113 FATE-HPPAAWKQLNDDYYIGDL-----AREEPLDELLKDY-RDMRAEFVREGLFKSSKA 164
 DB 60 FEDVGHTTTARAM-DEYYVGIDTSTIPARTKYVPPRQQBHYNQDKTPEFIIK----- 111
 Qy 165 WFLQLTINAAALFAASIATICYDKS 189
 DB 112 -ITQFLNPAILGLAVAIRYTKS 134
 RESULT 5
 CYB5_TOBAC STANDARD; PRT; 136 AA.
 ID CYB5_TOBAC STANDARD; PRT; 136 AA.
 AC P49098;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytochrome b5.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 OC NCBI_TaxID=4097;
 RN [1] RSEQUENCE FROM N.A.
 RP TISSUE=Leaf;
 RC MEDLINE=94325476; PubMed=8049375;
 RA Smith M.A., Stobart A.K., Shewry P.R., Napier J.A.;
 RT "Tobacco cytochrome b5: cDNA isolation, expression analysis and in vitro protein targeting.";
 RT Plant Mol. Biol. 25:527-537 (1994).
 CC FUNCTION: Cytochrome b5 is a membrane bound hemoprotein which function as an electron carrier for several membrane bound oxygenases. May play a key role in the modification by oxygenases. May play a key role in the modification by desaturation of fatty acids in the endoplasmic reticulum, which in the developing seed is utilized for membrane synthesis and in the developmentally regulated production of large amounts of storage lipids. Is involved in the reduction of cytochrome P-450 and may therefore be involved in flavonoid biosynthesis in the petals.
 CC SUBCELLULAR LOCATION: Microsomal membrane. Bound to the cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC TISSUE SPECIFICITY: Belongs to the cytochrome b5 family.
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 CC SIMILARITY: Belongs to the cytochrome b5 family.

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CC EMBL; X71441; CAA50575-1; ALT_INIT.
 CC EMBL; X68140; CAA48240-1; -.
 CC HSSP; P04166; 1B5M.
 DR InterPro; IPR00199; Cyt_B5.
 DR Pfam; PF00173; heme_1; 1.
 DR PRRTNS; PR00363; CYTOCHROMEBS.
 DR proDom; PD000612; Cyt_B5; 1.
 DR PROSITE; ES00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome;
 KW Multigene family.
 FT TRANSMEM 107 127 POTENTIAL.
 FT METAL 40 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 10 11 LA -> EF (IN REF. 1; CAA4B240).
 FT CONFLICT 105 105 MISSING (IN REF. 1; CAA4B240).
 SQ SEQUENCE 136 AA; 14979 MW; DACE93A695B2835F CRC64;

Query Match 6.9%; Score 179.5; DB 1; Length 136;
 Best Local Similarity 31.4%; Pred. No. 4.1e-08;
 Matches 43; Conservative 28; Mismatches 43; Indels 23; Gaps 6;

Qy 63 YSLADVA SHDRPGDCWMIVKYDISRFA DDHPGG-TVISTYFGRDGTDIVATEF-HPPA 120
 ::||::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 8 FTLAEVSOHNNNAKDCWLVISGKVYDVTKFLDDHPGGDEVLLSATGKD ATDDFEDVGHSSS 67

Qy 121 AWKQLNDYYIGDL-----AREEPLDELLKDY-RDMRAEF' REGLEFKSSKAWFLLQTLL 171
 |:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:
 Db 68 ARAMILDEYYXVGDEISATIPTKTYT PPNQ--PHYNQDKTSEFVVK-----LLQFL 115

Qy 172 INAAALLFAASIAATICYDX 188
 :||:||:||:||:
 Db 116 VPLIIIGVAFGIRFYTK 132

RESULT 6
 CYB5_CUSRE STANDARD; PRT; 135 AA.
 ID CYB5_CUSRE
 AC P49097;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome b5.
 OS Cuscuta reflexa (Southern Asian dodder).
 OC Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Convolvulaceae; Cuscuta.
 OX NCBI_TaxID=4129;
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95047507; PubMed=7959021;
 RA Subramanian K.; Mahadevan S.;
 RT "The cDNA sequence of cytochrome b5 associated with cytokinin-induced
 haustoria formation in *Cuscuta reflexa*.";
 RL Gene 149:375-376 (1994).
 CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases.
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane. Bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b5 family.

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DR HSSP; P04166; 1B5M.
 DR InterPro; IPR001199; Cyt_B5.
 DR PFam; PF00173; heme_1; 1.
 DR PRINTS; PR00363; CYTOCHROMEBS.
 DR PRODom; PD000612; Cyt_B5; 1.
 DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.
 DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.
 DR Electron transport; Transmembrane; Heme; Iron; Microsome;
 KW Multigene Family.
 KW Multigene Family.
 FT TRANSMEM 107 POTENTIAL.
 FT METAL 40 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT METAL 64 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 134 AA; 14869 MW; A36CCAD081A72ECBC CRC64;

Query Match 6.6%; Score 170.5; DB 1; Length 134;
 Best Local Similarity 28.8%; Pred. No. 2.3e-07;
 Matches 40; Conservative 36; Mismatches 38; Indels 25; Gaps 7;

Matches 30; Conservative 21; Mismatches 20; Indels 2; Gaps 2;

Qy 63 YSLADVASHDRPQDCWMIVKEKYDIDSRFADDHP-GGTIVISTYFGRDGTDVFATF-HPPA 120
 :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 8 FTLAEVSNHNNAKDCWNLISGKVYNVTXFLEDHPGGGEVLLSATGKDATDDFEDIGHSSS 67

Db 121 AWKQLNDYYIGDL--LDELLK-----DY-RDMRAEFVRREGLFKSSKAWFLLQT 170
 |:|||:|||:|||:|||:|||:|||:|||:
 68 AREMMEQQYYGEI---DPTTIPKKVKYTPPKQPHYNQDKTSSEFIK-----LLQF 114

Qy 171 LINAALFAASIAATICYDKS 189
 |:|||:|||:
 Db 115 LVPLATLGAVGIRIYTKS 133

RESULT 8
 CY52_ARATH STANDARD; PRT; 134 AA.

ID_048845; RESULT 9
 ID_NIA_LOTJA STANDARD; PRT; 900 AA.

AC P39869; SEQUENCE FROM N.A.
 DT 01-FEB-1995 (Rel. 31, Created)
 AC P39869; STRAIN=cv. Gifu / B-129;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE Probable cytochrome b5 isoform 2.
 DE Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 DE AT2G32720 OR F24L7.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicots; rosids;
 CC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 CC NCBI_TaxID=3702; [1]
 CX *Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounseley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Rostrine C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai S., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RL Nature 402:761-768(1999).
 CC -!- FUNCTION: Membrane bound hemoprotein which function as an electron
 CC carrier for several membrane bound oxygenases (By similarity).
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane. Bound to the
 CC cytoplasmic side of the endoplasmic reticulum (By similarity).
 CC -!- SIMILARITY: Belongs to the cytochrome b5 family.
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 CC EMBL; X80670; CAA56696.1; -.
 DR PIR; S47029; S47029.
 DR HSSP; P17571; 2CND.

flavoprotein pyridine nucleotide cytochrome reductases.";

RT C. Biol. Chem. 266:23542-23547(1991).

DR InterPro; IPR001199; Cyt_B5.

DR InterPro; IPR001834; Cyt_B5_reductase.

DR InterPro; IPR008335; Euk_Mb_oxred.

DR InterPro; IPR000833; FAD_binding_6.

DR InterPro; IPR0001709; FPN_cyt_reductse.

DR InterPro; IPR007110; Ig-Like.

DR InterPro; IPR005066; Mo-co_dimer.

DR InterPro; IPR005722; Oxidored_molyb.

DR InterPro; IPR001433; Oxred_FAD/NAD(P).

DR Pfam; PF00970; FAD_binding_6; 1.

DR Pfam; PF00173; heme_1; 1.

DR Pfam; PF03404; Mo-co_dimer; 1.

DR Pfam; PF00175; NAD_binding_1; 1.

DR Pfam; PF03174; Oxidored_molyb; 1.

DR PRINTS; PR00406; CYTB5RDTASE.

DR PRINTS; PR00363; CYTOCHROMEBS.

DR PRINTS; PR00407; EUROPTERIN.

DR PRINTS; PR00371; FPNCR.

DR ProDom; PD000612; Cyt_B5; 1.

DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.

DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.

DR PROSITE; PS00559; MOYBDOPTERIN_EUK; 1.

KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;

KW Nitrate assimilation.

FT METAL 172 172 MOYBDENUM-PTERIN (POTENTIAL).

FT METAL 226 226 MOYBDENUM-PTERIN (POTENTIAL).

FT DISULFID 411 411 INTERCHAIN (POTENTIAL).

FT METAL 556 556 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

FT METAL 579 579 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).

SQ SEQUENCE 900 AA; 101420 MW; 547C2538DD13535 CRC64;

Query Match 6.4%; Score 166.5; DB 1; Length 900;

Best Local Similarity 30.3%; Pred. No. 5.6e-06;

Matches 46; Conservative 20; Mismatches 63; Indels 23; Gaps 5;

QY 3 LVTDLFNLFLGTTWSKYSVTH---SYAGNYGPTLKHAKKVSA---GKTAGQTLRQRSVQD 57

Db 446 LIVNVMMNNNCW---FRVKTNWCKPHKGEIGIVFEHPTQPGNQPGGMKAERHLIESQOD 5C3

QY 58 KK2----GTYSLADVASHDRPGDCMWIKERKVYDISRFADHPGGT-VI 1c1

Db 504 SRPIIKKSVSSPPFMNTFTKMYSLSEVKKHNSPDSAWIIVHGHWYDCTRFLKDHPGGADSI 563

QY 102 STYFGGRGTDVATFHPPAAWKQLNDYYIGDL 133

Db 564 LINAGTDCTEEEFPFHSDKAKKMLEDYRGEL 595

RESULT 10

ID	NIA_CUCMMA	STANDARD	FRT	918 AA.
AC	P17569;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Nitrate reductase [NADH] {EC 1.7.1.1} (NR).			
OS	Cucurbita maxima (Pumpkin) (Winter squash).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid I; Cucurbitales; Cucurbitaceae; Cucurbita.			
NCBI_TaxID	3661; [1]			
RN	SEQUENCE FROM N.A.			
RP	Crawford N.M., Campbell W.H., Davis R.;			
RC	TISSUE=Seedling;			
RX	MEDLINE=92084635; Pubmed=1748631;			
RA	Hyde G.E., Crawford N.M., Campbell W.H.;			
RT	"The sequence of squash NADH:nitrate reductase and its relationship to the sequences of other flavoprotein oxidoreductases. A family of			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8073-8076(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	Crawford N.M., Campbell W.H., Davis R.;			
RT	Nitrate reductase from squash: cDNA cloning and nitrate regulation."			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8073-8076(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Seedling;			
RX	MEDLINE=92084635; Pubmed=1748631;			
RA	Hyde G.E., Crawford N.M., Campbell W.H.;			
RT	"The sequence of squash NADH:nitrate reductase and its relationship to the sequences of other flavoprotein oxidoreductases. A family of			

Query Match 6.3%; Score 164; DB 1; Length 918;

Best Local Similarity 30.3%; Pred. No. 9.4e-06;

Matches 46; Conservative 22; Mismatches 60; Indels 24; Gaps 6;

QY 3 LYTDFLNFLGTTWSKYSVTH---SYAGNYGPTLKHAKKVSA---GKTAGQTLRQRSVQD 57

Db 469 LIVNLGMNNNCW---FRVKTNWCKPHKGEIGIVFEHPTQPGNQPGGMKAERHLIESQOD 5C3

QY 47 GOTLRQRSV---QDKKP GTSLADVASHDRPGDCMWIKERKVYDISRFADHPGGT-VI 1c1

Db 527 NQTLK-KSVSTPEMNTASNTYLSEVKKHNSPDSAWIIVHGHWYDCTRFLKDHPGGSDSI 585

QY 102 STYFGGRGTDVATFHPPAAWKQLNDYYIGDL 133

Db 586 LINAGTDCTEEEFPFHSDKAKKMLEDYRGEL 617

RESULT	12	FD3D_ARATH	STANDARD;	EPT;	435 AA.
FT DOMAIN	192	196	HISTIDINE BOX-2.		
FT DOMAIN	359	363	HISTIDINE BOX-3.		
SQ SEQUENCE	435 AA;	50136 MW;	3D77A8035A6214E1	CRC64;	
Query Match	6.3%	Score 162.5; DB 1;	Length 435;		
Best Local Similarity	20.4%;	Pred. No. 4.9e-06;			
Matches 105;	Conservative 66;	Mismatches 180;	Indels 163;	Gaps 25;	
QY	18 YSVYTHSYAGNYGPTLK-----HAKKVSAGQKTAGOTIQRQSVQD 57				
DB	18 YPKHTTSEASNPKPTEFKENPPLKPPSSLNSRYGFYSKTRNWALNVATPLTTIQSPEED 77				
QY	58 KK-----PGTYSLADVASHDRPGDCWMMIVKEKVYDISRFADDHPGGTVISTYFGRDGTD 111				
DB	78 TERFDPGAPPENLAIR-AIPKHCW-----VAIVFGL--AA 126				
QY	112 VPATFHPPAWKQLNDYYIGIDLAREEPLDELLKDYRDMRAEFVREGGLPKSSKAWFLQLCTL 172				
DB	127 VAAYFNNWLLW-----PL-----YWFQAQGTM 147				
QY	172 INAALEFAASATICCYDKSYWAVILSASLMGLFVQQCGWLAKHDFLHQQVFENRTANSFFGY 231				
DB	148 -----FWA-----LFW-----LGHDCCGHGSFSNDPRLNNSVAGH 175				
QY	232 LEGNCVLFGSVSWMWRTRKHNIHHTAPN--ECDEQXYTPLDEDIDTLPIIAWSKEJLAVESK 289				
DB	176 LLHSSIL-VPYHGWREISHRTBHQNNGHVNDESWHELPESI-----YKNLEKTTQ-- 224				
QY	290 RILRVLQYQHYMILPLLPMARYSW--TFGSILLFENPDLSTTKGLIEKGTVAFHYAWFSSW 347				
DB	225 -----MERFTLPFPMLAYPFYLWNRSPGKQGSHYHPPDSDFLPLKEKKDVLTSTACWTAM 278				
QY	348 AAFHE-LPGVAKPLA-----WVATELVAGLLLGFYFTLSSHNGKE----VYNESK 392				
DB	279 RALLVCLNFWMGPQIMKLGYGIPWIFV-----M9LDFVTYLHHHGHDKLPLWYRKEW 332				
QY	393 DFVRAQWITTRNTKRGWFDWFTGGLDTQIEHHLFPTMPRHNPYKIAPOVEALCKKHGLE 452				
DB	333 SYLRGG-LTTLDRDYGWNN-IHDIGTHVHHLFPOIIPHILVEATEAKPVUGKTYRE 390				
SEQUENCE FROM N.A.					
STRAIN=cv.	Columbia;	TISSUE=Aerial parts;			
MEDLINE=95148742;	PubMed=7846164;				
Gibson S., Arondel V., Iba K., Somerville C.R.;	"Cloning of a temperature-regulated gene encoding a chloroplast omega-3 desaturase from Arabidopsis thaliana.";				
Submitted (SEP-1993); to the EMBL/GenBank/DBJ databases.					
[1]					
SEQUENCE FROM N.A.					
STRAIN=cv.	Columbia;	TISSUE=Hypocotyl;			
Watahiki M.C., Yamamoto K.T.;					
Submitted (SEP-1993); to the EMBL/GenBank/DBJ databases.					
[13]					
SEQUENCE FROM N.A.					
STRAIN=cv.	Columbia;				
MEDLINE=97471969;	PubMed=9330910;				
Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M., Miyajima N., Tabata S.;	"Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned P1 clones.",				
DNA Res. 4:215-230(1997).					
- - FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol.					
- - PATHWAY: Polyunsaturated fatty acid biosynthesis.					
- - SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).					
- - INDUCTION: BY LOW TEMPERATURE.					
- - DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.					
- - SIMILARITY: Belongs to the fatty acid desaturase family.					
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CC DR EMBL; L27158; AAA65621.1; -.					
CC DR EMBL; U08216; AAB63302.1; -.					
CC DR EMBL; D17578; BAA04504.1; -.					
CC DR EMBL; AB005241; BAB11547.1; -.					
CC DR InterPro; IPR005804; FA_desat_fam.					
CC DR Pfam; PF03497; FA_desatrase; 1.					
CC DR ProDom; PDC01081; FA_desat_fam; 2.					
CC DR Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane; Transit peptide.					
CC CC TRANSIT 1 ? CHLOROPLAST (POTENTIAL).					
CC CC CHAIN ? 435 TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE.					
CC CC DOMAIN 156 160 HISTIDINE BOX-1.					

-!- INDUCTION: By nitrate.	SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
-!- SIMILARITY: TO EUKARYOTIC MOLYBDOPTERIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.		
-!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.		
-!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.		
EMBL; XE4136; CAB45497.1; -.		
PIR; JC1422; JC1422.		
DR HSSP; P04166; 1B5M.		
DR InterPro; IPR001199; Cyt_B5.		
DR InterPro; IPR001834; Cyt_B5_reductase.		
DR InterPro; IPR008335; Euk_Mb_oxred.		
DR InterPro; IPR008333; FAD_binding_6.		
DR InterPro; IPR0017C9; FPN_cyt_redctse.		
DR InterPro; IPR0017C9; Ig-Tike.		
DR InterPro; IPR005066; Mo-co_dimer.		
DR InterPro; IPR000572; Oxidored_molyb.		
DR InterPro; IPR001433; Oxred_FAD/NAD(P).		
Pfam; PF03370; FAD_binding_6; 1.		
Pfam; PF03173; heme_1; 1.		
Pfam; PF03404; Mo-co_dimer; 1.		
Pfam; PF00175; NAD_binding_1; 1.		
Pfam; PF00174; oxidored_molyb; 1.		
PRINTS; PRO00406; CYTB5RDIASE.		
PRINTS; PR00363; CYTCEROMEBS.		
PRINTS; PR00407; EUMCPTERIN.		
PRINTS; PR00371; FPNCR.		
PRODom; PDC00612; Cyt_B5; 1.		
PROSITE; PS00191; CYTOCHROME_B5_1;		
PROSITE; PS50255; CYTOCHROME_B5_2;		
PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.		
Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;		
Nitrate assimilation.		
METAL 139 139 MOLYBDENUM-PTERIN (POTENTIAL).		
METAL 193 193 MOLYBDENUM-PTERIN (POTENTIAL).		
DISULFID 376 376 INTERCHAIN (POTENTIAL).		
METAL 532 532 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).		
METAL 555 555 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).		
SEQUENCE 864 AA; 96402 MW; 499529652CDDDL1C7 CRC64;		
Query Match 6.2%; Score 160.5; DB 1; Length 864;		
Best Local Similarity 40.0%; Pred. No. 1.7e-05;		
Matches 32; Conservative 11; Mismatches 36; Indels 1; Gaps 1;		
60 PGTYSLADVASHDRPGDCWMIKEKVYDLSRFADDHPGGT-VISTYFGRGTDVFAFEHHP 118		
497 PROYTMEEVAAHNTTEESCWVHGKVTATPYLDEHPGGAESILIVAGADATDEFNSIHS 556		
119 PAWKQLNDYYIGDLAREEP 138		
557 SKAKAMLRQYYIGDLVASKP 576		
RESULT 13		
ID CYB5_YEAST STANDARD; PRT; 120 AA.		
ID P40312; AC		
DT 01-FEB-1995 (Rel. 31, Created)		
DT 01-OCT-1996 (Rel. 34, Last sequence update)		
DT 28-FEB-2003 (Rel. 41, Last annotation update)		
DE Cytochrome b5.		
EN CYB5 OR YNL11C OR N1949.		
DS Saccharomyces cerevisiae (Baker's yeast).		
DS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		

NIA2_PHAU	STANDARD;	PRT;	890 AA.	Gaps	6;
ID P39866;					
AC DT 01-FEB-1995 (Rel. 31; Created)					
CC DT 01-FEB-1995 (Rel. 31; Last sequence update)					
CC DT 28-FEB-2003 (Rel. 41; Last annotation update)					
DE Nitrate reductase [NADH] 2 (EC 1.7.1.1) (NR-2).					
GN NIA2 OR MR2.					
OS Phaseolus vulgaris (Kidney bean) (French bean)					
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eudicots I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.					
OC NCBI_TaxID=3885;					
OX RN [1]					
RP STRAIN=cv. Saxa;					
RA Jensen P.E., Hoff T., Stummwolff B.M., Henningsen K.W.;					
RL Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.					
CC -!- FUNCTION: Nitrate reductase is a key enzyme involved in the first step of nitrate assimilation in plants, fungi and bacteria.					
CC -!- CATALYTIC ACTIVITY: Nitrite + NAD(+) + H(2)O = nitrate + NADH.					
CC -!- COFACTOR: Requires FAD, a heme group (called cytochrome b-557) and one molybdenum atom.					
CC -!- SUBUNIT: Homodimer. (By similarity).					
CC -!- SIMILARITY: TO EUKARYOTIC MOLYBDOPERTIN OXIDOREDUCTASES IN THE N-TERMINAL DOMAIN.					
CC -!- SIMILARITY: Contains 1 cytochrome b-5 heme-binding domain.					
CC -!- SIMILARITY: TO FAD/NAD-BINDING CYTOCHROME REDUCTASES IN THE C-TERMINAL DOMAIN.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
CC EMBL; U01029; AAA95940.1; .					
DR PIR; TI1805; T11805.					
DR HSPP; PI7571; 2CND.					
DR InterPro; IPR001199; Cyt_B5.					
DR InterPro; IPR001834; Cyt_B5_reductase.					
DR InterPro; IPR008335; Euk_Mb_oxred.					
DR InterPro; IPR009333; FAD_binding_6.					
DR InterPro; IPR001709; FPN_cyt_reductse.					
DR InterPro; IPR007110; Ig-Like.					
DR InterPro; IPR00566; Mo-co_dimer.					
DR InterPro; IPR000572; Oxidored_molyb.					
DR InterPro; IPR001433; Oxred_FAD/NAD(P).					
DR Pfam; PF00970; FAD_binding_6; 1.					
DR Pfam; PF00173; heme_1; 1.					
DR Pfam; PE03404; Mo-co_dimer; 1.					
DR Pfam; PF00175; NAD_binding_1; 1.					
DR Pfam; PF00174; oxidored_molyb; 1.					
DR PRINTS; PR004406; CYTB5RDTASE.					
DR PRINTS; PR00363; CYTOCHROMEBS.					
DR PRINTS; PR00407; EUROMOPTERIN.					
DR PRINTS; PR00371; FPNCR.					
DR ProdDom; PDD00612; Cyt_35; 1.					
DR PROSITE; PS00191; CYTCEROME_B5_1; 1.					
DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.					
DR PROSITE; PS00559; MOLYBDOPERTIN_EUK; 1.					
KW Oxidoreductase; Flavoprotein; FAD; NAD; Heme; Molybdenum;					
KW Nitrate assimilation; Multigene family.					
FT METAL 165 165 MOLYBDENUM-PTERIN (POTENTIAL).					
FT METAL 219 219 INTERCHAIN (POTENTIAL).					
FT DISULFID 404 404 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).					
FT METAL 548 548 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).					
FT METAL 571 571 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).					
SQ SEQUENCE 890 AA; 99995 MW; FCC3B96F0139DE1 CRC64;					
Query Match 6.24; Score 160; DB 1; Length 890;					
SQ 380 AA; 43996 MW; 1C005117A8DAE16B CRC64;					

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Query Match      6.1%; Score 159.5; DB 1; Length 380;
Best Local Similarity 23.0%; Pred. No. 7.4e-06;
Matches 77; Conservative 48; Mismatches 137; Indels 73; Gaps 16;

QY  148 DMRAEFVREGLEK-----SKAWEFLQLTLINAAALFAASIACTICYDKSYWAIVLASAS---LNG 201
Db   34 DIRAAIPKHCKWEEKSTLRSLSYVLRDVLVTTALAASAISFNSW--FFWPPLYWPAQGTMEWA 91

QY  202 LFVQQCGWLAHDFLIHQOVFENRTANSFFGYLFGNCCVWLGFESVSWRTKHNIIHTAPN--EC 259
Db   92 LFV----LGHDCGHGSFSNSKLNSFVGHILHSLIL-VPYNGWRISHRTHQNHGHWEK 145

QY  260 DEQYTPLDEDIDTLPIIAWSKEILLATVESKRILRLVQYQHYMILPLLFMARYSW--TEGS 317
Db  146 DESWVPLTE-----KVYXNLLED--MTRMLRYS--FPPIPFAYPFYLNWRSPGK 189

QY  318 LLFTFNPDLSTTKGLIEKGTVAFHYAKFSWAFAHILPGVAKPLAWMVATELVAG---- 371
Db  190 EGSHENPYSNLFPSPGERKGVVTSILCW----GIV--LSVLLYLSITIGPIFMILK 237

QY  372 -----LLIGFVFTLSSHNGKEYVNEKDFVRAQV-----ITTRTRKRGWENDWF 414
Db  238 LYGVPYLIFVNMWLDFVTYLLHHG--YTAKLPWYRGQEWSYLRGGLTWDRDYGINN-V 293

QY  415 TGGLDTQIEHHLFPTMPRENYEKLAPQEALCKKH 449
Db  294 EHDIGTHVIIHLPFPQIPHHRWEATKSAKSVLGKY 328

```

Search completed: June 16, 2004, 19:06:19
 Job time : 19 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 16, 2004, 19:06:22 ; Search time 46 Seconds
{without alignments}
3312.941 Million cell updates/sec

Title: US-09-980-468-2
Perfect score: 2595
Sequence: 1 MALVTDLFNLGTTWSKV.....AVVKALKEIAADEASIRLHAA 483

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : SPTRXMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodont:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

SPTRXMBL_25:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2595	100.0	483	10	Q9LENO		Q91en0 ceratodon p
2	1619	52.4	520	10	Q9LEM9		Q91em9 ceratodon p
3	1475	56.8	525	10	Q9ZNW2		Q9znw2 physcomitrium
4	841.5	32.4	457	3	Q9UUV3		Q9uvv3 mortierella
5	840.5	32.4	457	3	Q8X173		Q8x173 mortierella
6	839.5	32.4	457	3	Q9UTY3		Q9uty3 mortierella
7	835.5	32.2	457	3	Q9HEY4		Q9hey4 mortierella
8	821.5	31.7	457	3	Q8X174		Q8x174 mortierella
9	821.5	31.7	457	3	Q9HEY1		Q9hey1 mortierella
10	799.5	30.8	477	10	Q8RXYB0		Q8rxbo phaeodactylus
11	79.6	30.4	459	10	Q944W4		Q944w4 pythium irreg
12	743.5	28.7	458	3	Q7Z8P2		Q7z8p2 rhizopus sp
13	705.5	27.2	467	3	Q96VC3		Q96vc3 mucor circinelloides
14	668.5	25.8	357	3	Q9HDF4		Q9hdf4 helianthus annuus
15	603.5	23.3	458	10	Q43469		Q43469 helianthus annuus
16	587	22.6	449	10	Q92RP7		Q92rp7 arabidopsis

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3

Result No.	Score	Query	Match	Length	DB	ID	Description
1	2595	100.0	483	10	Q9LENO		Q91en0 ceratodon purpureus
2	1619	52.4	520	10	Q9LEM9		Q91em9 ceratodon purpureus
3	1475	56.8	525	10	Q9ZNW2		Q9znw2 physcomitrium
4	841.5	32.4	457	3	Q9UUV3		Q9uvv3 mortierella
5	840.5	32.4	457	3	Q8X173		Q8x173 mortierella
6	839.5	32.4	457	3	Q9UTY3		Q9uty3 mortierella
7	835.5	32.2	457	3	Q9HEY4		Q9hey4 mortierella
8	821.5	31.7	457	3	Q8X174		Q8x174 mortierella
9	821.5	31.7	457	3	Q9HEY1		Q9hey1 mortierella
10	799.5	30.8	477	10	Q8RXYB0		Q8rxbo phaeodactylus
11	79.6	30.4	459	10	Q944W4		Q944w4 pythium irregularis
12	743.5	28.7	458	3	Q7Z8P2		Q7z8p2 rhizopus stolonifer
13	705.5	27.2	467	3	Q96VC3		Q96vc3 mucor circinelloides
14	668.5	25.8	357	3	Q9HDF4		Q9hdf4 helianthus annuus
15	603.5	23.3	458	10	Q43469		Q43469 helianthus annuus
16	587	22.6	449	10	Q92RP7		Q92rp7 arabidopsis

SEQUENCE FROM N.A.
STRAIN=wt3; TISSUE=Protonemata;
MEDLINE=20307617; PubMed=10848999;
-|- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
CC EMBL; AJ250734; CAB94992.1; -.
DR HSSP; PC4166; 1B5M.
DR GC; GO:00016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase_1.
DR Pfam; PF00173; heme_1_1.
DR ProdDom; PDD00612; Cyt_B5_1.
DR ProdDom; PDD01081; FA_desat_fam_2.
DR PROSITE; PS50255; CYTOCHROME_B5_2_1.
KW Heme.
RN [1] SEQUENCE FROM N.A.
RL Eur. J. Biochem. 267:3801-3811(2000).
RC MEDLINE=20307617; PubMed=10848999;
RX Sperling P., Lee M., Girke T., Zaehringer U., Stymne S., Heinz B.;
RT "A bifunctional delta 6-fatty acyl acetyl enolese/desaturase from the
RT moss Ceratodon purpureus (MCBS).
OS Ceratodon purpureus (MCBS).
OC Bryopsida; Dicranidae; Dicranales; Ceratodontidae; Ceratodon.
OX NCBI_TaxID=3225;
RN [1] SEQUENCE FROM N.A.
RC STRAIN=wt3; TISSUE=Protonephridia;
RX MEDLINE=20307617; PubMed=10848999;
RA Sperling P., Lee M., Girke T., Zaehringer U., Stymne S., Heinz B.;
RT "A bifunctional delta 6-fatty acyl acetyl enolese/desaturase from the
RT moss Ceratodon purpureus. A new member of the cytochrome b5
RT superfamily.";
RR Eur. J. Biochem. 267:3801-3811(2000).
CC -|- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
DR EMBL; AJ250734; CAB94992.1; -.
DR HSSP; PC4166; 1B5M.
DR GC; GO:00016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR001199; Cyt_B5.
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase_1.
DR Pfam; PF00173; heme_1_1.
DR ProdDom; PDD00612; Cyt_B5_1.
DR ProdDom; PDD01081; FA_desat_fam_2.
DR PROSITE; PS50255; CYTOCHROME_B5_2_1.
KW Heme.
SQ SEQUENCE 483 AA; 54857 MW; C451D042169AB1C2 CRC64;

Query Match 100.0%; Score 2595; DB 10; Length 483;
Best Local Similarity 100.0%; Pred. No. 5.4e-217;
Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q9LEM9		Best Local Similarity 61.5%; Pred. No. 4.8e-132; Matches 302; Conservative 72; Mismatches 101; Endels 16; Gaps 3;	
QY	1 MALVTDLFNLFLGTTWSKSYVTHSYAGNYGPTLKHAKKVSAQGKTAGQTLLRORSVQDKKP 60	QY	1 MALVTDLFNLFLGTTWSKSYVTHSYAGNYGPTLKHAKKVSAQGKTAGQTLLRORSVQDKKP 60
Db	1 MALVTDLFNLFLGTTWSKSYVTHSYAGNYGPTLKHAKKVSAQGKTAGQTLLRORSVQDKKP 60	QY	1 MALVTDLFNLFLGTTWSKSYVTHSYAGNYGPTLKHAKKVSAQGKTAGQTLLRORSVQDKKP 60
QY	61 GTYSLADVAHDRPGDCWMIVKEKYDISRFADDHPGGTVISTYGRDGTDVEATFHPPA 120	Db	25 MPLVSDFNLFLGTTQMSLST-TFAFKRLTICKHSSDISVEAQKESVARGPVENT-SQSV 83
Db	61 GTYSLADVAHDRPGDCWMIVKEKYDISRFADDHPGGTVISTYGRDGTDVEATFHPPA 120	QY	47 GOTLRQRQSVQDKKPGTYSLADVAHDRPGDCWMIVKEKYDISRFADDHPGGTVISTYFG 106
QY	121 AWKQLNDYYIGDLDAREEPLDELLKDYRDRAEFVREGLFKSSKAWFLQTLINAALFALS 180	Db	84 AQPIRRWRWQDKKPKVTSLKDVAASHDMPQDCWIIKEKVYC-STFAEQHEGGTVINTYFG 143
Db	121 AWKQLNDYYIGDLDAREEPLDELLKDYRDRAEFVREGLFKSSKAWFLQTLINAALFALS 180	QY	107 RDGTDVFATEHPPAAWKQNLNDYYIGDLDAREEPLDELLKDYREMRAEFVREGLFKSSKAWF 166
QY	181 IATICYDKSYWAIVLVSASLMGLFVQQCGWLAHDFLHQOVFENRTANSFFGYLFGNCVULGF 240	Db	144 RDATDVFESTPHASTSWKILQNFYIGNLVREBPTLELLKEYRELRAFLREQLFRKSXSY 203
Db	181 IATICYDKSYWAIVLVSASLMGLFVQQCGWLAHDFLHQOVFENRTANSFFGYLFGNCVULGF 240	QY	167 LLQTLINAAALPAASIAITCYDKSYWAIVLVSASLMGLFVQQCGWLAHDFLHQQVFPENRTAN 226
QY	241 SVSWMWRTKHNIHTHATAPNECDEQTYTPLDEDIDTLPITLAWSKELIATVESKRILRVQYQHY 300	Db	204 LFKTLLINVSIVATSIAITSLYKSYRAVLLSASLMGLFVQQCGWLSHDFLHQVFEETRWLN 263
Db	241 SVSWMWRTKHNIHTHATAPNECDEQTYTPLDEDIDTLPITLAWSKELIATVESKRILRVQYQHY 300	QY	227 SFFGYLSGNCVYLGFPSVSMWRTKHNIHTHATAPNECDEQTYTPLDEDIDTLPITLAWSKELIATV 286
QY	301 MILPLLFMARYSWTFGSSLFTENPDLSSTKGLIEKGTVAFHYAWFSWALPHILPGVAKPL 360	Db	264 DVUGYVWGVNVVLGFPSVSMWRTKHNIHTHATAPNECDEQTYTPLDEDIDTLPITLAWSKELIATV 323
Db	301 MILPLLFMARYSWTFGSSLFTENPDLSSTKGLIEKGTVAFHYAWFSWALPHILPGVAKPL 360	QY	287 ESKRILRVLQYOHYMLPPLLFMARYSWTFGSSLFTENPDLSSTKGLIEKGTVAFHYAWFS 346
QY	361 AWWVATELVAGLILGFVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGMFNDWFTGGLDT 420	Db	324 ESKTMRLRVLQYQHLFFVLLTFAKRSWLFWSAAFTLRELTGEKLLERGTMAHLHYIWFN 383
Db	361 AWWVATELVAGLILGFVFTLSSHNGKEVYNESKDFVRAQVITTRNTKRGMFNDWFTGGLDT 420	QY	347 WAAFHILPGVAKPLAMMVALEYAGLILGFVFTLSSHNGKEVYNESKDFVRAQVITTRNTK 406
QY	421 QIEHHLFTPMBRHNYPKIAPOQWEALCKHGLEYDNVSVGASVAVRALKIAADEASIRL 480	Db	384 SVAFYLLPG-WKPVVVWWVSELMSGFLLGYYVFLVSHNGMEVYNTSKDFVNQAQIASTRDIK 442
Db	421 QIEHHLFTPMBRHNYPKIAPOQWEALCKHGLEYDNVSVGASVAVRALKIAADEASIRL 480	QY	407 RGWFNDWFTGGLDTQIEHHLFTPMBRHNYPKIAPOQWEALCKHGLEYDNVSVGASVAVV 466
QY	481 HAH 483	Db	443 AGVFENDWFTGGLNRQIEHHLFTPMBRHNLNKISPHVETLCKHGLEYDNVSVGASVAVV 502
Db	481 HAH 483	QY	467 KALKEIAADEAS 477
		Db	503 KTLDKVADAAAS 513
RESULT 2			
Q9LEM9 PRELIMINARY; ERT; 520 AA.			
ID	Q9LEM9;	RESULT 3	Q9ZNW2
AC	Q9LEM9;	ID	Q9ZNW2
DT	01-OCT-2000 (TREMBLrel. 15, Created)	AC	Q9ZNW2;
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	DT	01-MAY-1999 (TREMBLrel. 10, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE	Delta 6-fatty acid desaturase	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
OS	Ceratodon purpureus (Moss)	DE	DE DELTA6-acyl-lipid desaturase.
OC	Bryopsida; Viridiplanteae; Streptophyta; Bryophyta; Ceratodon.	GN	GN DES6.
OC	Dicranidae; Dicranales; Funariales; Physcomitrella patens (Moss)	OS	Physcomitrella patens (Moss).
OX	NCBI_TaxID=3225;	OC	Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariidae; Funariales; Physcomitrella patens.
OX	NCBI_TaxID=3225;	OC	NCBI_TaxID=3218;
RN	[1]	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=wt3; TISSUE=Protonemata;	RC	STRAIN=HEDW. B. S. G;
RX	RT	RX	MEDLINE=9B416756; PubMed=9744093;
RX	RT	RA	Girke T.; Schmidt R.; Zaehringer U.; Reski R.; Heinz E.;
RX	RT	RT	*Identification of a novel delta 6-acyl-group desaturase by targeted gene disruption in Physcomitrella patens.";
RX	RT	RT	Plant J. 15:39-48 (1998).
RX	RT	RL	- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.
RX	RT	RL	EMBL: AJ22981; CAA11C33.1; -.
RX	RT	DR	EMBL: AJ22980; CAA11032.1; -.
RX	RT	DR	HSSP; P04166; LICC.
RX	RT	DR	GO; GO:0016491; F:oxidoreductase activity; IEA.
RX	RT	DR	InterPro; IPR001199; Cyt B5.
RX	RT	DR	InterPro; IPR005804; FA_desat_fam.
RX	RT	DR	InterPro; IPR005804; FA_desat_fam.
RX	RT	DR	Pfam; PF00487; FA_desaturase_1.
RX	RT	DR	Pfam; PF00173; heme_1; 1.
RX	RT	DR	ProDom; PD000612; Cyt B5; 1.
RX	RT	DR	ProDom; PD001081; FA_desat_fam; 2.
RX	RT	DR	ProSite; PS50255; CYTOCHROME_B5_2; 1.
KW	Heme.	DR	ProSite; PS50255; CYTOCHROME_B5_2; 1.
SQ	SEQUENCE 520 AA; 59160 MW; SA9332EECC153439 CRC64;	DR	DR
Query Match	62.4%; Score 1619; DB 10; Length 520;	DR	DR

KW	Heme.	DR	Pfam;
SQ	SEQUENCE	DR ProdOm; PD000612; Cyt_B5;	PF00173; heme_1; 1.
		DR ProdOm; PD001081; FA_desat_fam;	CytoCHROME_B5_1; 1.
	Query Match	DR PROSITE; PS00191; CYTOCHROME_B5_1; 1.	
	Best Local Similarity	DR PROSITE; PS50255; CYTOCHROME_B5_2; 1.	
	Matches 281; Conservative 74; Mismatches 117; Indels 36; Gaps 6;	KW Heme.	
Qy	1 MALVTDNFLNGLTT---WSKYSVYTHSYAGNYGPTLKHAKKVS-----43	SEQUENCE 457 AA; DR D90169E86911450A CRC64;	
Db	25 MSLFSDFFSYSSSTGWSVHSIQPLK----RLTSKKRVSSEAAVOCISAEVQRNSS 77	Query Match 32.4%; Score 841.5%; DB 3; Length 457;	
Qy	41 -----AQKTAGQTLRQRSVQDKPPTGTYSLADVASHDRCDCWMIVKEKVYDISRPAID 94	Best Local Similarity 39.2%; Pred. No. 1.8e-64;	
Db	78 TGTAAEALAESVVVKPTRLRSQWK-KSTHPLSEWAENKPSDCWIVVKNKVYDVSNFADE 136	Mismatches 72; Matches 177; Conservative 177;	
Qy	95 HPGGTIVISTTYFGRDGTDFVATEHPPAAWKQQLNDYYIGJDLAREEPLDELLKDYRDMDRAEFTV 154	Indels 43; Gaps 10;	
Db	137 HPGGSVISTTYFGRDGTDFVATEHPPAAWKQQLNDYYIGJDLAREEPLDELLKDYRDMDRAEFTV 154	Qy 62 TYSLADV-----ASHDPRPGDCWMIVKEKVYDISRFAADDHPGGTVISTYFGRDGTDFV 113	
Qy	155 REGLFKSSKAWEPLLQTLINAALEFAASIACTTCYDKSYWAIVLSSAISMLFVOCGWLAHDF 214	Db 9 TETRAEVLNEALNEGKXDAEAPFLMIIDNKNVYDIREFVDPDHPGGSVILTHVGKDGTDFV 68	
Db	197 REQLFKSSKLYYVAKLITNVAFIAASIACTTCYDKSYWAIVLSSAISMLFVOCGWLAHDF 214	Qy 114 ATFPPEPAWKQQLNDYYIGJDL---AREEPPLDELLKDYRDMDRAEFTVREGGLEFKSSKAWEPLLQTL 170	
Qy	215 LHQQVFENRTANSFFGTYLFGNCYLSWTRTKHNIHHTAPNECDEQYTPLDEDIDTLP 274	Db 69 DTFHPERAWETLANFYVGDIEDSRDIKNDFAAEVRKLRTLFOSLGYDSSSKAYAYAFKV 128	
Db	257 LHNVQFETRWLNEWVGGVIGNAVLGFSTGWWKKBKHNLHHAAPNECDQTYQPIDEDIDTLP 316	Qy 171 LINAALFAASIACTYC-DKSYWAIVLSSAISMLFVOCGWLAHDF 196	
Qy	317 LIAWSKIDILATVENKTELRILQYQHLEPMGLLEFARGSWLFWSWRTYSTAVLS PVDRLLE 376	Db 129 SENLCIWGSLSTVIAKGQQTSTLAVNVISSAALLGLFWOQCGWLAHDFLHHHQVFQDRFWGDL 188	
Db	335 KGTVAFHAYAWFSNAAFHILPGVAKPLAMMVALTELVAGLLLGFVFTLSEHNGKEVYNE 394	Qy 229 FGYLFGNCVLFGSVSWWRTKHNIHHTAPNECDEQYTPLDEDIDTLPILAWSK---EILAT 285	
Qy	377 KGTVLFHYFWFVGTACYLPG-WKPLVWMAVTTELMSGMLLGFWVLSHNGMEVYNSKEF 435	Db 193 EGAFLGGVCOQGFSSSWWKD-XHNTTHAAEPNVEGE-----DPDIDTHPLLTSEHALEMFS 243	
Db	395 VRAQVITTRNTKGWFNDWFTGGLDTQIEHHLFPTMPHRNYPKIAPOVEALC 446	Qy 286 VESKRILRVLQYQHYMIL-----PLLFMARYSWTFGSLLFTFNPDLSITK-----330	
Qy	436 VSAQIVSTRDIKGNIENDWFTGGLNRQIEHHLFPTMFRHNLNKTAAPREVFCRKHGLVYE 495	Db 244 VPDEELTRM--WSREMVINQTHFFPILSARLISWLQSIILFVL-PNGQAHKPSGARVPI 300	
Db	455 NVSVVGASVAVVKALEIADEASIRIHA 492	Qy 331 GLIEKGTVAFHYAWFSNAAFHILPGVAKPLAMMVALTELVAGLLLGFVFTLSEHNGKEVYNE 390	
Qy	496 DVSIATGICKVTKVALKALKEVA-EAAAEEQHA 522	Db 301 SLEVQLSLAMEHWWTWYLATMTMELFLIKDPVNMLVYFLVSQAVCGNLLAIVFSLNENGMPVISK 360	
Db		Qy 391 SK----DFVRAQVITTRNTKGWFNDWFTGGLDTQIEHHLFPTMPHRNYPKIAPOVEALC 446	
		Db 361 EEAVIDMDFFFTKQIITGRDVHPGLFANWFTGGLNYGIEHHLFPMSPRHFNSKIQPAVETLC 420	
		Qy 447 KKHGLEYDNNVSVVGSVAVVKALEIADEAS 477	
		Db 421 KKYNVRYHTGMIEGTAEVFSRNLNEVSKAAS 451	
RESULT 4			
Q9UVV3	ID Q9UVV3 PRELIMINARY; PRT; 457 AA.	Q9X173 PRELIMINARY; PRT; 457 AA.	RESULT 5
AC	Q9UVV3: ID Q8X173.	AC Q8X173.	Q9X173
DT	01-MAY-2000 {TREMBLrel. 13, Created)	DT 01-MAR-2002 {TREMBLrel. 20, Created)	SEQUENCE FROM N.A.
DT	01-MAY-2000 {TREMBLrel. 13, Last sequence update)	DT 01-MAR-2002 {TREMBLrel. 20, Last sequence update)	DR GO:0016491; F:oxidoreductase activity; IEA.
DT	01-JUN-2003 {TREMBLrel. 24, Last annotation update)	DT 01-JUN-2003 {TREMBLrel. 24, Last annotation update)	DR InterPro: IPR001199; Cyt_B5.
DE	Delta-6 fatty acid desaturase.	DE Delta-6 fatty acid desaturase.	DR InterPro: IPR005804; FA_desat_fam.
OS	Mortierella alpina.	OS Mortierella isabellina (Umbelopsis isabellina).	DR Pfam: PF00487; FA_desaturase; 1.
Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;	OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;	OC Mucorales incertae sedis; Umbelopsis.	DR NCBITaxID=91625; NCBI_TaxID=91625; [1]
OC Mortierellaceae; Mortierellaceae;	OC Mortierellaceae; Mortierellaceae;	OC Mortierellaceae; Mortierellaceae;	DR GO:0016491; F:oxidoreductase activity; IEA.
OX NCBI_TaxID=64518;	OX NCBI_TaxID=64518;	OX NCBI_TaxID=64518;	DR InterPro: IPR001199; Cyt_B5.
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	DR InterPro: IPR005804; FA_desat_fam.
RC STRAIN=ATCC32221;	RC STRAIN=M6-22;	RC Xing L., Liu L., Li M., Hu G.;	DR Pfam: PF00487; FA_desaturase; 1.
RX MEDLINE=99406036; PubMed=10478922;	RA Huang Y.S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,	RA "Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella isabellina M6-22 genomic and cDNA.";	DR InterPro: IPR001199; Cyt_B5.
RA Cha S.M., Kirchner S.J., Mukerji P., Knutzon D.S.;	RA "Cloning of delta 12- and delta 6-desaturases from Mortierella alpina and recombinant production of gamma-linolenic acid in Saccharomyces cerevisiae.";	RA Submitted (JAN-2002) to the EMBL/GenBank/DDJB databases.	DR InterPro: IPR001199; Cyt_B5 FAMILY.
RT DE Delta-6 fatty acid desaturase.	RT DE Delta-6 fatty acid desaturase.	RT DE Delta-6 fatty acid desaturase.	DR EMBL: AF465282; AAL73948.1; -.
OS Mortierella alpina.	OS Mortierella isabellina (Umbelopsis isabellina).	OS Mortierella isabellina (Umbelopsis isabellina).	DR GO:0016491; F:oxidoreductase activity; IEA.
RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	RN SEQUENCE FROM N.A.	DR HSSP; P04166; IEUE.
RC AF110510; AAF08685.1; -.	RC GO; GO:0016491; F:oxidoreductase activity; IEA.	RC GO; GO:0016491; F:oxidoreductase activity; IEA.	DR InterPro: IPR001199; Cyt_B5.
DR HSSP; P04166; IEUE.	DR InterPro: IPR001199; F:oxidoreductase activity; IEA.	DR InterPro: IPR001199; Cyt_B5.	DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR001199; F:oxidoreductase activity; IEA.	DR InterPro: IPR001199; F:oxidoreductase activity; IEA.	DR InterPro: IPR001199; Cyt_B5.	DR InterPro: IPR001199; Cyt_B5.
DR InterPro: IPR005804; FA_desat_fam.	DR InterPro: IPR005804; FA_desat_fam.	DR InterPro: IPR005804; FA_desat_fam.	DR InterPro: IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.	DR Pfam; PF00487; FA_desaturase; 1.	DR Pfam; PF00487; FA_desaturase; 1.	DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD000612; Cyt_B5; 1.	DR ProDom; PD000612; Cyt_B5; 1.	DR ProDom; PD000612; Cyt_B5; 1.	DR ProDom; PD000612; Cyt_B5; 1.

DR	ProDom; PD001081; FA_desat_fam; 2.	DR	ProDom; ED001081; FA_desat_fam; 2.
DR	PRCSITE; PS00191; CYTOCHROME_B5_1; 1.	DR	PRCSITE; PS00191; CYTOCHROME_B5_1; 1.
DR	PRCSITE; PS50255; CYTOCHROME_B5_2; 1.	DR	PRCSITE; PS50255; CYTOCHROME_B5_2; 1.
KW	Heme.	RW	Heme.
SQ	SEQUENCE 457 AA; 51784 MW;	SQ	SEQUENCE 457 AA; 51816 MW; 5C4B3D7312439543 CRC64;
Query	79 MIVKEKVDISRFADDHPGGTVISTYFGRDGTDVATFHPPADWKQLNDYYIGDLAREEP 138	Query	79 MIVKEKVDISRFADDHPGGTVISTYFGRDGTDVATFHPPADWKQLNDYYIGDLAREEP 138
Db	34 YIDNKKVYDVREFVDPHGGSWLTHVGKDTDVFDTFHPEAAWETLANFYVGIDESDR 93	Db	34 YIDNKKVYDVREFVDPHGGSWLTHVGKDTDVFDTFHPEAAWETLANFYVGIDESDR 93
Query	139 L---DELLKDYRDMDRAEFVREGFLFKSSKAWEILQTLINNALFAASIATICY--DKSYWAI 193	Query	139 L---DELLKDYRDMDRAEFVREGFLFKSSKAWEILQTLINNALFAASIATICY--DKSYWAI 193
Db	94 AIKNDDFAAEVRKLRTLFQSLGYSKAYAFAKVSFNLCIWIGLSTFIVAKWGTSTLAN 153	Db	94 AIKNDDFAAEVRKLRTLFQSLGYSKAYAFAKVSFNLCIWIGLSTFIVAKWGTSTLAN 153
Query	194 VLSASIMGLEFVOCQGWLHAHDFLEHQOVFENRTANSFFGYLFGNCVLGFSVSWWRTKHNIHH 253	Query	194 VLSASIMGLEFVOCQGWLHAHDFLEHQOVFENRTANSFFGYLFGNCVLGFSVSWWRTKHNIHH 253
Db	154 VLSAALLGLFWOOCQGWLHAHDFLEHQVFDRLFGAFLGGVCQGFSSWWKDGHNTHH 213	Db	154 VLSAALLGLFWOOCQGWLHAHDFLEHQVFDRLFGAFLGGVCQGFSSWWKDGHNTHH 213
Query	254 TAPNECDEQYTPLEEDIDTLPLIAWSK--EILATEVKRILVQHQYHML---- 303	Query	254 TAPNECDEQYTPLEEDIDTLPLIAWSK--EILATEVKRILVQHQYHML---- 303
Db	214 AAPNVHGE----DPDIDTHPLLTWSEHALEMPSCTPDEELTRM--WSREMVLNQTWEYF 266	Db	214 AAPNVHGE----DPDIDTHPLLTWSEHALEMPSCTPDEELTRM--WSREMVLNQTWEYF 266
Query	304 PILLFMARYSWTFGSLLFTENPDLSSTK----GLIEKGTVAFHYAWFSAWFHILPG 355	Query	304 PILLFMARYSWTFGSLLFTENPDLSSTK----GLIEKGTVAFHYAWFSAWFHILPG 355
Db	267 PILSFARLSWCLOSILFVL-PNGQAHKPSSGARVPISLVEQLSLLAVHWTMFLFIKD 325	Db	267 PILSFARLSWCLOSILFVL-PNGQAHKPSSGARVPISLVEQLSLLAVHWTMFLFIKD 325
Query	356 VAKPLAWMVAATEVAGLLIGFVFTLSHNGKEVYNESK----JFTRAQVITTRNTKRGWMN 411	Query	356 VAKPLAWMVAATEVAGLLIGFVFTLSHNGKEVYNESK----JFTRAQVITTRNTKRGWMN 411
Db	326 PVNMIVYFLVSCAQCGNLLAIVFSLNHNGMPVISKEAVDMDFFTKOITGRDVHPGLFA 385	Db	326 PVNMIVYFLVSCAQCGNLLAIVFSLNHNGMPVISKEAVDMDFFTKOITGRDVHPGLFA 385
Query	412 DWFTGGLDTQIEHHLEPTMPRHNPYKTAPOVEALCKEGLEYDNVVSGASVAVVKALKE 471	Query	412 DWFTGGLDTQIEHHLEPTMPRHNPYKTAPOVEALCKEGLEYDNVVSGASVAVVKALKE 471
Db	386 NWFTGGLNYQIEHHLEPSMPRHNFSKIOPAVEVTSKQAVETLCKYGVRYHTTGMIETGAEVPSRLNE 445	Db	386 NWFTGGLNYQIEHHLEPSMPRHNFSKIOPAVEVTSKQAVETLCKYGVRYHTTGMIETGAEVPSRLNE 445
Query	472 IADEAS 477	Query	472 IADEAS 477
Db	446 VSKAAS 451	Db	446 VSKAAS 451
RESULT 6			
Q9UVY3	PRELIMINARY; STRAIN=1S-4;	PRT;	457 AA.
ID	Q9UVY3	ID	Q9HEY4
AC	Q9UVY3;	AC	Q9HEY4;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	"Delta-6 fatty acid desaturase"	DE	"Delta-6-fatty acid desaturase."
OS	Mortierella isabellina (Umbelopsis isabellina)	OS	Mortierella isabellina (Umbelopsis isabellina)
OC	Eukaryota; Fungi; Zygomycetes; Zygomycetes; Mucorales;	OC	Eukaryota; Fungi; Zygomycetes; Zygomycetes; Mucorales;
OC	Mucorales incertae sedis; Umbelopsis.	OC	Mucorales incertae sedis; Umbelopsis.
OX	NCBI_TaxID=64518;	OX	NCBI_TaxID=91625;
RN	[1]	RN	[1]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	RA	Ming-Chun, L.; Li, L.; Guo-Wu, H.; Li, Z.; Lai-Jun, X.;
RX	MEDLINE=20035749; PubMed=10570972;	RA	"Cloning and sequencing analysis of delta6-fatty acid desaturase gene from Mortierella isabellina."
RA	Sakuradani E., Kobayashi M., Shimizu S.;	RT	Junwu Xitong 0:0-0 (2001).
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DE	Mortierella isabellina (Umbelopsis isabellina).
RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	OS	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
CC	Mortierellaceae; Mortierella.	CC	Mucorales incertae sedis; Umbelopsis.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=91625;
DR	[1]	DR	[1]
DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
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RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	DR	SEQUENCE FROM N.A.
CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
DR	[1]	DR	[1]
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RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
RX	MEDLINE=20035749; PubMed=10570972;	DR	SEQUENCE FROM N.A.
RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
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CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
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DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
RX	MEDLINE=20035749; PubMed=10570972;	DR	SEQUENCE FROM N.A.
RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	DR	SEQUENCE FROM N.A.
CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
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RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
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RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	DR	SEQUENCE FROM N.A.
CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
DR	[1]	DR	[1]
DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
RX	MEDLINE=20035749; PubMed=10570972;	DR	SEQUENCE FROM N.A.
RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	DR	SEQUENCE FROM N.A.
CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
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RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
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RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
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CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
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DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
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RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
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DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
DR	[1]	DR	[1]
DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
RX	MEDLINE=20035749; PubMed=10570972;	DR	SEQUENCE FROM N.A.
RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
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CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
DR	[1]	DR	[1]
DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
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RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	DR	SEQUENCE FROM N.A.
CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
DR	[1]	DR	[1]
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RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
RX	MEDLINE=20035749; PubMed=10570972;	DR	SEQUENCE FROM N.A.
RA	Sakuradani E., Kobayashi M., Shimizu S.;	DR	SEQUENCE FROM N.A.
RT	"Delta 6-fatty acid desaturase from an arachidonic acid-producing Mortierella fungus. Gene cloning and its heterologous expression in a Mortierella alpina.	DR	SEQUENCE FROM N.A.
RT	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;	DR	SEQUENCE FROM N.A.
CC	Mortierellaceae; Mortierella.	CC	Mortierellaceae; Mortierella.
DR	NCBI_TaxID=64518;	DR	NCBI_TaxID=64518;
DR	[1]	DR	[1]
DR	SEQUENCE FROM N.A.	DR	SEQUENCE FROM N.A.
RC	STRNAME=1S-4;	DR	SEQUENCE FROM N.A.
RX	MEDLINE=20035749; PubMed=10570972;	DR	SEQUENCE FROM N.A.
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KW	SEQUENCE	Heme.	457 AA;	51772 MW;	668E7EB21172D5AF CRC64;	Query Match 32.2%; Score 835.5; DB 3; Length 457; Best Local Similarity 40.1%; Pred. No. 5.8e-64; Matches 171; Conservative 70; Mismatches 150; Indels 35; Gaps 9;	Query Match 31.7%; Score 821.5; DB 3; Length 457; Best Local Similarity 39.9%; Pred. No. 9.6e-63; Matches 170; Conservative 70; Mismatches 151; Indels 35; Gaps 9;
Qy	79 MIYKEKVDISRFADDHPGGTIVISTYFGRDGTDVATFHPPAAWKQLNDYYIGDOLAREEP	Qy	79 MIYKEKVDISRFADDHPGGTIVISTYFGRDGTDVATFHPPAAWKQLNDYYIGDOLAREEP	138	138	139 L--DELLKDYRDMRAEFVREGLEFKSSKAFFLQLTINALFAASIAITCY--DKSYWAI	193
Db	34 MIIDNKVYDVRETFPDHPGSWILTHVGKDTDVFDFTFPEAAWETLANFTVGDIEDESDR	Db	34 MIIDNKVYDVRETFPDHPGSWILTHVGKDTDVFDFTFPEAAWETLANFTVGDIEDESDR	93	93	94 AIKNDDFAAEVVKLRLTLEQSLGYYDVSKAFFLQLTINALFAASIAITCY--DKSYWAI	193
Qy	139 L--DELLKDYRDMRAEFVREGLEFKSSKAFFLQLTINALFAASIAITCY--DKSYWAI	Qy	139 L--DELLKDYRDMRAEFVREGLEFKSSKAFFLQLTINALFAASIAITCY--DKSYWAI	193	193	94 AIKNDDFAAEVVKLRLTLEQSLGYYDVSKAFFLQLTINALFAASIAITCY--DKSYWAI	193
Db	94 AIKNDDFAAEVVKLRLTLEQSLGYYDVSKAFFLQLTINALFAASIAITCY--DKSYWAI	Db	94 AIKNDDFAAEVVKLRLTLEQSLGYYDVSKAFFLQLTINALFAASIAITCY--DKSYWAI	193	193	94 AIKNDDFAAEVVKLRLTLEQSLGYYDVSKAFFLQLTINALFAASIAITCY--DKSYWAI	193
Qy	194 VLSASLMGLFVQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	Qy	194 VLSASLMGLFVQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	253	253	194 VLSASLMGLFVQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	253
Db	194 VLSASLMGLFVQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	Db	194 VLSASLMGLFVQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	253	253	194 VLSASLMGLFVQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	253
Qy	154 VLSAALLGLFWQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	Qy	154 VLSAALLGLFWQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	213	213	154 VLSAALLGLFWQQCGWLAHDFLHQVQFENRTANSFFGYLFQNCVULGFSVSUWRTKHNHH	213
Db	254 TAPNECDEQYTPLDEDIDTLPLIANSK---EILATVESKRILRVLQYQHYML---	Qy	254 TAPNECDEQYTPLDEDIDTLPLIANSK---EILATVESKRILRVLQYQHYML---	303	303	254 TAPNECDEQYTPLDEDIDTLPLIANSK---EILATVESKRILRVLQYQHYML---	303
Qy	214 AAPNVHGE----DPDIDTHPLLTWSEHALEMFSDVDPDEELTRM--WSREMVLNOTWYIF	Db	214 AAPNVHGE----DPDIDTHPLLTWSEHALEMFSDVDPDEELTRM--WSREMVLNOTWYIF	266	266	214 AAPNVHGE----DPDIDTHPLLTWSEHALEMFSDVDPDEELTRM--WSREMVLNOTWYIF	266
Db	304 PILLMARYSWTFGSSLFLFPNPDLSSTK-----GLIEKGTVAFHYAWFSAFAHILECG	Qy	304 PILLMARYSWTFGSSLFLFPNPDLSSTK-----GLIEKGTVAFHYAWFSAFAHILECG	355	355	304 PILLMARYSWTFGSSLFLFPNPDLSSTK-----GLIEKGTVAFHYAWFSAFAHILECG	355
Db	267 PILSFARLSWCLQSILLYL-PNGQAHKPSGARVTSISLYEQLSLAMHWWTWYLATMFLFIKD	Db	267 PILSFARLSWCLQSILLYL-PNGQAHKPSGARVTSISLYEQLSLAMHWWTWYLATMFLFIKD	325	325	267 PILSFARLSWCLQSILLYL-PNGQAHKPSGARVTSISLYEQLSLAMHWWTWYLATMFLFIKD	325
Qy	356 VAKPLAKWVATELVAGLLGFVETLSSHNGKEVYNESK---DFVRAQVITTRNTKRGWMFN	Qy	356 VAKPLAKWVATELVAGLLGFVETLSSHNGKEVYNESK---DFVRAQVITTRNTKRGWMFN	411	411	356 VAKPLAKWVATELVAGLLGFVETLSSHNGKEVYNESK---DFVRAQVITTRNTKRGWMFN	411
Db	326 PVNNMMVVYFLVNSQAVCGNLLIAVFSNLNHNGMPVTSKEEAVDMDEFKQIITGRDWHPGLFA	Qy	326 PVNNMMVVYFLVNSQAVCGNLLIAVFSNLNHNGMPVTSKEEAVDMDEFKQIITGRDWHPGLFA	385	385	326 PVNNMMVVYFLVNSQAVCGNLLIAVFSNLNHNGMPVTSKEEAVDMDEFKQIITGRDWHPGLFA	385
Qy	412 DWFTGGGLDTQIEHHLFPTMPRHNTYKLAPOVEALCKKHGLEYDNVSVGASHVYVKALKE	Db	412 DWFTGGGLDTQIEHHLFPTMPRHNTYKLAPOVEALCKKHGLEYDNVSVGASHVYVKALKE	471	471	412 DWFTGGGLDTQIEHHLFPTMPRHNTYKLAPOVEALCKKHGLEYDNVSVGASHVYVKALKE	471
Db	386 NWFTGGLNQYIEHHLFPPSMRHNFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLINE	Qy	386 NWFTGGLNQYIEHHLFPPSMRHNFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLINE	445	445	386 NWFTGGLNQYIEHHLFPPSMRHNFSKIQPAVETLCKKYGVRYHTTGMIEGTAEVFSRLINE	445
Qy	472 IADEAS 477	Db	472 IADEAS 477	451	451	472 IADEAS 477	451
Db	446 VSKAAS 451	Db	446 VSKAAS 451			446 VSKAAS 451	
RESULT 9							
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AC	Q9HEY1;	Q9HEY1;					
DT	01-MAR-2001 (TREMBLrel. 16, Created)	DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DE	Delta 6-fatty acid desaturase.				
DE	Delta 6 fatty acid desaturase.	GN	Mortierella alpina				
GN	Mortierella alpina	OS	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;				
OS	Mortierellaceae; Mortierella.	OC	Mortierellaceae; Mortierella.				
OC	Mortierella alpina.	OX	Mortierella alpina.				
CX	NCBI_TaxID=64518;	RN	SEQUENCE FROM N.A.				
RN	[1]	Q8X174	PRELIMINARY;	PRT;	457 AA.		
ID	Q8X174;	Q8X174;					
AC	Q8X174;	Q8X174;					
DT	01-MAR-2002 (TREMBLrel. 20, Created)	DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DE	Delta 6-fatty acid desaturase.				
DE	Delta 6 fatty acid desaturase.	GN	Mortierella alpina				
GN	Mortierella alpina	OS	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;				
OS	Mortierellaceae; Mortierella.	OC	Mortierellaceae; Mortierella.				
CX	NCBI_TaxID=64518;	RN	SEQUENCE FROM N.A.				
RN	[1]	Q8X174	PRELIMINARY;	PRT;	457 AA.		
ID	Q8X174;	Q8X174;					
AC	Q8X174;	Q8X174;					
DT	01-MAR-2002 (TREMBLrel. 20, Created)	DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)				
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	DE	Delta 6-fatty acid desaturase.				
DE	Delta 6 fatty acid desaturase.	GN	Mortierella alpina				
GN	Mortierella alpina	OS	Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;				
OS	Mortierellaceae; Mortierella.	OC	Mortierellaceae; Mortierella.				
CX	NCBI_TaxID=64518;	RN	"Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA."				
RN	[1]	Q8X174	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.				
CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.	RC	"Cloning and sequence analysis of the delta 6 fatty acid desaturase gene from Mortierella alpina ATCC16266 genomic and cDNA."				
DR	DR GO:0016491; F:oxidoreductase activity; IEA.	RC	"Expressed in Mortierella cerevisiae."				
DR	InterPro; IPR001199; Cyt B5.	RC	Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.				
DR	InterPro; IPR005804; FA_desat_Fam.	CC	-!- SIMILARITY: BELONGS TO THE CYTOCHROME B5 FAMILY.				
DR	PFam; PF00487; FA_desat_Fam;	DR	EMBL; AF307940; RAG45092.1; -.				
DR	PFam; PF00173; heme_1; 1.	DR	EMBL; AF465283; AAL73949.1; -.				
DR	ProDom; PDD000612; Cyt B5; 1.	DR	HSSP; P04166; LEUE.				
DR	ProDom; PDD001081; FA_desat_Fam;	DR	DR GO:0016491; F:oxidoreductase activity; IEA.				
DR	PROSITE; PS00191; CYTOCHROME_B5_1; 1.	DR	InterPro; IPR005804; FA_desat_Fam.				
DR	PROSITE; PS550255; CYTOCHROME_B5_2; 1.	DR	InterPro; IPR001199; Cyt B5.				
KW	Heme.	SQ	InterPro; PF003487; FA_desat_Fam.				
KW	SEQUENCE 457 AA;	SQ	PFam; PF00173; heme_1; 1.				
KW	SEQUENCE 51772 MW;	SQ	PFam; PF00173; heme_1; 1.				


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Query Match      23.3%;   Score 603.5;   DB 10;   Length 458;
Best Local Similarity    31.1%;   Pred. No. 8.9e-44;
Matches 136;   Conservative 85;   Mismatches 193;   Indels 23;   Gaps 8;

Qy  54  SVQDKKPSTYSLADJWASHDRPSIDCANNIVKEKVDISRFADDHPG3GTY-1STYGRDGTDV 112
Db  11  SIADGKKYITS-KELKKHNNPNDLWISILGKVINVTEAKEHPGGDAPLINLAGQDVTA 69

Qy  113  FATEHPPAAWKQLNDYYIGDLAREEPLDELLKDYRDMRAEFVREGLPKSSKAWFLLQTLI 172
Db  70  FIAFHPTGTAWKHLDKLFGTGYHLKDYQVSIDSIRDYRKLAASEFAKAGMFEKKGHGVYSLCF 129

Qy  173  NAALFAASIAATICYDKSYWAIWUSASLIMGLFVQQCGWLAHDFLHQVFEENTRANSFFCYL 232
Db  130  VSLLLSACVYGVLYSGSFWIHMLSGAILGLAAMQIAYLGHDAHYQMMATRGWNKPGIF 189

Qy  233  FGNCVLGEFSVSWWRTRCHNHTAPNECDEQYTPLDEDIDLPLZIAWSKEILATESKRIL 292
Db  190  IGNCITGISIAWWKWTNAHHIACNSDL---YCPDLQHLPMLAVSSKLFNSITSVFG 244

Qy  293  RVL-----QYCHYMLPULLMARYSWTFGSLIFTNPDLSTTKGLIEKGTVAFHY 342
Db  245  RQLTFDPLARFFVSYCHLYYPIMCVARVNLYLQTILLISKRKIPDRGLNLIGTLIF-W 303

Qy  343  AWFSWAEEHILPGVAKPLAMWVATELVAGLLLGFVFTLISHNGKEVY--NESKDFVRAQV 399
Db  304  TWFPPLLVR-LPNWPERVAFLVSYFCVTG-TQHIQFTLNHFSGDVYVGPPKGDNWEEKQF 361

Qy  400  ZTTRNTKRGWENDWFTGGLDTQIEHHLFPTMRENYPKIAQPQEALCKKHGLEYDNVSVV 459
Db  362  RGTTIDIACSSWMDWFEGGLQFQLEHHLFPRLRCHLRSISPICRELCKKYNLPVSLSFY 421

Qy  460  GASVAVVKALKEIADEA 476
Db  422  DANVTTLKTLRTAALQA 438

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Search completed: June 16, 2004, 19:10:42
 Job time : 49 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 19, 2004, 02:36:30 ; Search time 3746 Seconds

(without alignments)
 3850.356 Million cell updates/sec

SUMMARIES

	Result No.	Score	Query Match	Length	DB ID	Description
Title:	C 1	652	25.1	753	12	BJ579910
Perfect score:	C 2	649	25.0	764	12	BJ169984
Sequence:	C 3	634	24.4	688	12	BJ170744
Scoring table:	C 4	617	23.8	728	12	BJ597842
BLOSUM62	C 5	583	22.5	697	12	BJ599570
Xgapop 10.0 , Xgapext 0.5	C 6	583	22.5	698	12	BJ604593
Ygapop 10.0 , Ygapext 0.5	C 7	567.5	21.9	1764	11	AY1C3762
Fgapop 6.0 , Fgapext 7.0	C 8	53.9	20.8	519	12	BQ040185
Delop 6.0 , Delex 7.0	C 9	52.9	20.4	2272	11	AK076485
Searched:	C 10	52.8	20.3	1335	29	AY418548
27513289 seqs, 14931090276 residues	C 11	527.5	20.3	3318	11	AK083959
Total number of hits satisfying chosen parameters:	C 12	517	19.9	622	10	AW476747
Minimum DB seq length: 0	C 13	516	19.9	1689	11	AK080414
Maximum DB seq length: 2000000000	C 14	514	19.8	3129	11	AK029318
Post-processing: Minimum Match 0%	C 15	503	19.4	1335	29	AY418550
Maximum Match 100%	C 16	499	19.2	746	12	BJ583356
Listing first 45 summaries	C 17	479	18.5	766	12	BJ600861
Minimum DB seq length: 0	C 18	478	18.4	3697	11	AK090042
Maximum DB seq length: 2000000000	C 19	443.5	17.1	699	12	BJ597953
Post-processing: Minimum Match 0%	C 20	443.5	17.1	703	12	BJ599342
Maximum Match 100%	C 21	443.5	17.1	726	12	BJ603698
Listing first 45 summaries	C 22	441.5	17.0	1131	29	AY420234
Command line parameters:	C 23	439	16.9	2862	11	AK083282
-MODEL=frame+p2n.model -DEV=x1h	C 24	438	16.9	480	12	BJ599078
-Q=/cgn2_1/uspto_spool/us09980468/runat_16062004_174742_27187/app_query.fasta_1.647	C 25	428.5	16.5	1131	29	AY420236
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LIST=0	C 26	409	15.8	522	12	BJ601553
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45	C 27	409	15.8	985	14	CB264523
-DOCALIGN=B 200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGNN=15 -MODE=LOCAL	C 28	401.5	15.5	1079	29	AY420235
-OUTFILE=pto NORM=ext HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000	C 29	392.5	15.1	507	12	BJ173747
-USER=US09980468 @CGN_1.1_3437 @runat_16062394_174742_27187 -NCPU=6 -ICPU=3	C 30	382	14.7	867	29	CG847823
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG	C 31	377	14.5	721	13	BQ864828
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6	C 32	376	14.5	696	13	BQ861565
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7	C 33	375	14.5	786	14	CD837141
Database :	C 34	373.5	14.4	721	14	CB972537
EST: *	C 35	370.5	14.3	934	29	CG264599
1: em_estba:*	C 36	368	14.2	748	13	BQ976973
2: em_esthum:*	C 37	367.5	14.2	817	14	CB893839
3: em_estin:*	C 38	366	14.1	756	13	BU025934
4: em_estru:*	C 39	364.5	14.0	651	13	BO409001
5: em_estov:*	C 40	364.5	14.0	914	29	CG463170
6: em_estpl:*	C 41	363	14.0	922	29	CG238209
7: em_estro:*	C 42	361	13.9	655	13	BU026750
8: em_htc:*	C 43	359	13.8	745	13	BU026884
9: gb_est1:*	C 44	359	13.8	765	13	BU024179
10: gb_est2:*	C 45	357.5	13.8	427	10	AW699009
11: gb_htc:*						Y
12: gb_est3:*						
13: gb_est4:*						
14: gb_est5:*						
15: em_estfun:*						
16: em_estom:*						
17: em_gss_hum:*						
18: em_gss_inv:*						
19: em_gss_pln:*						
20: em_gss_vrt:*						
21: em_gss_fut:*						
22: em_gss_mam:*						
23: em_gss_mus:*						
24: em_gss_pro:*						
25: em_gss_rod:*						
26: em_gss_phg:*						
27: em_gss_vrl:*						
28: em_gssi:*						

ALIGNMENTS

RESULT 1	BU579910/c	753 bp mRNA linear EST 22-OCT-2003
LOCUS	BU579910	normalized full length cDNA library, chloronemata, caulinemata and malformed buds Physcomitrella patens subsp. patens cDNA clone pphb12117 3', mRNA sequence.
DEFINITION		
VERSION	BU579910	EST.
KEYWORDS		
SOURCE	Physcomitrella patens subsp. patens	
ORGANISM	Physcomitrella patens subsp. patens	Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Funariae; Funariales; Funariidae; Funariaceae; Physcomitrella; Bryopsida;

REFERENCE	1 (bases 1 to 753)	572 GTTCTGTTCACTTTCGTCGGACAGCGGTATCTCCCTGGT---TGG 516	
AUTHORS	Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.	358 LysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeuGlyPheVal 377	
TITLE	Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution	515 AAGCATTAGTAGTATGGTGGACTGGTGCATGGCATTGTCGGCATGGCTTGTA 456	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)	QY	
MEDLINE	22709184	Db	
PUBMED	12808149	QY	
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp	Db	
	A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FUC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XbaI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector(5'-GAGAGAGAGATCCAACCTCTGGAGATGCTGTTCCAGACAGACGCCGNNNN-3' was used as a 1st 3' primer, and 5'-ggRTTCGAGTCATCGTGTGGCTGAGCTGATGACTCGAGCGATGACTCGAGAACTGGAATGGCCGAGCTCGAATTCTCGAGAAACCG). CDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).	QY	
	Prctonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCObase (http://moss.nibb.ac.jp).	Db	
FEATURES	Location/Qualifiers	RESULT 2 BJ169984/c	
	source	LOCUS	
	/organism="Physcomitrella patens subsp. patens"	BJ169984	
	/mol_type="mRNA"	764 bp mRNA linear EST 16-OCT-2003	
	/sub_species="patens"	DEFINITION	
	/db_xref="taxon:145482"	BJ169984 full length cDNA library, chloronemata and young gametophores Physcomitrella patens subsp. patens cDNA clone pph24e05 3', mRNA sequence.	
	/clone="pphb1211"	ACCESSION	
	/tissue_type="mixture of chloronemata, caulonemata and malformed buds"	BJ169984	
	/clone_lib="normalized full length cDNA library, chloronemata, caulonemata and malformed buds"	VERSION	
		EST	
		KEYWORDS	
		SOURCE	
		ORGANISM	
		Physcomitrella patens subsp. patens	
		Eukaryota; Streptophyta; Embryophyta; Bryophyta;	
		Bryopsida; Funariales; Funariaceae; Physcomitrella.	
		REFERENCE	
		1 (bases 1 to 764)	
		AUTHORS	
		Nishiyama,T., Fujita,T., Shin-i,T., Seki,M., Nishide,H., Uchiyama,I., Kamiya,A., Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe,M.	
		TITLE	
		Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution	
		PROC. NATL. ACAD. SCI. U.S.A. 100 (13), 8007-8012 (2003)	
		JOURNAL	
		22709184	
		MEDLINE	
		12808149	
		COMMENT	
		Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855	
		Email: tshini@genes.nig.ac.jp	
		A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FUC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XbaI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector(5'-gAGAGAGAGATCCAACCTCTGGTATTTCGCTGGTAGTTGGAGAACTGGAATCCACCTGGTCTCATGGGTCTGTTGGCTCTGGAGCT 633 was used as a 1st 3' primer, and 5'-ggRTTCGAGTCATCGTGTGGCTGAGCTGAGCTGAGAACTGGAATCCACCTGGTCTCATGGGTCTGTTGGTAGTTGGCTCTGGAGCT 633 was used as a 2nd 5' -hairpin primer, giving the following 5' boarder sequence, AGGCCAAATGGCCGAGCTCGAATTCTCGAGCTGAGAAACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).	
		ORIGIN	
		Alignment Scores:	
		Pred. No.: 2-48e-68	Length: 753
		Score: 652.00	Matches: 126
		Percent Similarity: 73.56%	Conservative: 25
		Best Local Similarity: 61.46%	Mismatches: 52
		Query Match: 25.13%	Indels: 2
		DB: 12	Gaps: 2
		US-09-980-468-2 (1-493) x BJ169910 (1-753)	
		QY	278 TrpSerLysGluLeuAlaThrValGluSerLysArgIleLeuArgValLeuGlntry 297
		Db	752 TGAGGCAAGGACATACTGGCCACAGTGAAGATAAGACATTCTCCAAATAC 693
		QY	298 GlnHistoyrMetIleLeuProLeuLeuProAspLeuSerThrThrLysGlyLeuLeuGlyLysGlyThr 317
		Db	692 CAGCATCTGTTCTCATGGTCTGTTGGCTCTGGTAGTTGGCTCTGGAGCT 633
		QY	318 LeuLeuPheHistoyrAlaTrpSerAspLeuSerThrThrLysGlyLeuLeuGlyLysGlyThr 337
		Db	632 TGGAGATAACCTCTACAGCAGTGTCTCACCTGTGACAGGTGTTGGAGAAGGGAACT 573
		QY	338 ValAlaPheHistoyrAlaTrpSerTrpAlaAlaPheHisIleLeuProGlyvalAla 357

rottonemata were blended by the POLYTRON, and then cultivated on BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/Eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCOBase (<http://moss.nibb.ac.jp>).

Location/Qualifiers

1. 764

/organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"
 /sub_species="patens"
 /db_xref="taxon:145481"
 /clone="pph24e05"
 /tissue_type="mixture of chloronemata and young gametophores with 2 to 5 leaves"
 /clone_lib="full length cDNA library, chloronemata and young gametophores"

RESULT	EST	688 bp	mRNA linear	EST 16-OCT-2003
LOCUS	BJ170744	688 bp	chloronemata and young	
DEFINITION	BJ170744	full length cDNA library,	Physcomitrella patens	physcomitrella patens cDNA clone
		gamtophores	subsp.	ppn26120 3'
ACCESSION	BJ170744			mRNA sequence.
VERSION	BJ170744.1	GI:18338720		
KEYWORDS	EST.			
SOURCE	Physcomitrella patens subsp. patens			
ORGANISM	Physcomitrella patens subsp. patens			
REFERENCE	Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella			
AUTHORS	Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Hayashizaki, Y., Shinozaki, K., Uchiyama, I., Kamiya, A., Carninci, P., Kohara, Y., and Hasebe, M.			
TITLE	Comparative genomics of Physcomitrella patens gametophytic transcriptionome and Arabidopsis thaliana: implication for land plant evolution			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)			
MEDLINE	22709184			
PUBMED	12808149			
COMMENT	Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855			
E-mail:	tshini@genes.nig.ac.jp			
5.91e-68	Length: 764			
64.9.00	Matches: 127			
73.56%	Conservative: 26			
61.06%	Mismatches: 53			
25.01%	Indels: 2			
12	Gaps: 2			
-09-980-468-2 (1-483) x BJ169984 (2-764)				
275 IleLeuAlaTrpSerLysGluIleLeuAlaThrValGluSerLysArgIleLeuArgVal 294				
762 CTCATTGCCTGNAGCAGGACATACTGGCACACAGTTGAGAATHAGCATCTTGGCAATC 703				
295 LeuGlnTyrglnHistYMetIleLeuProLeuLeuPheMethIlaargTyrsTerTpThr 314				
702 CTCCAATACCAGCATCTGTTCTCATGGGTCTGTATTTCGCCGTGGTAGTTGGCTC 643				
315 PheGlyserLeuLeuPheThrPheAsnProAspLeuSerThrIhrLysGlyLeuIleGlu 334				
642 TTTGGAGCTGGAGATAATACCTCTACAGCACGGTGTGGAG 583				
335 LysGlyThrvalAlaPheHisYrrAlaTrpPheSerTerTpAlaPheHisIleLeuPro 354				
582 AAGGAAACTGTTCTGTTCACTACTTGGTCTGTTCTCCCT 523				
355 GlyValAlaLysProLeuAlaTrpMetValAlaThrGlyLeuLeuLeu 374				
522 GGT---TGGAGGCCATTAGTAGATGGGTGACTGAGCTCATGTCTGCTG 466				
375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPhe 394				
465 GGCTTTGTTGTTACTTAGGCCACAATGGGATGGCGTTATAATTTCGTCATAAGAATTTC 406				
395 ValArgAlaGlnValIleThrArgAsnThrLysArgGlyLysGluSerLysAspTrpPhe 414				
405 GTGAGTGACAGATCGTATCCACACGGGATATCAAAGGAACATATTCAACGACTGGTC 346				
415 ThrglyglyLeuAspThrGlnIleGluHisHisLeuPheProArgHisAsn 434				
345 ACTGGTGGCCTAACAGGCAAATAGGCTCATCTTCCAACAAATGCCCAAGGCATAT 286				
435 TyrProLysIleAlaProGlnValIleLeuCysLysLysHisGlyLeuGlutYasp 454				
285 TTAACAAATAGCACCTAGAGTGGAGGTGTTCTGTAAGAACACGGTCTGGTGTACGAA 226				
455 AsnValSerValValGlyAlaSerValAlaValValLysGlyIleAlaAsp 474				
225 GACGTATCTGCTACTGGCACACTGGCAAGGTTTGAAGGAAGTCGCGC--- 169				
475 GluAlaserIleArgIleUHisAla 482				
168 GAGGCTGGCAGAGCAGCATGCTACTGGCACACTGGCAAGGTTTGAAGGAAGTCGCGC--- 145				
US-09-980-468-2 (1-483) x BJ170744 (1-688)				
279 SerLysIuIleLeuAlaThrValGluSerLysArgIleLeuGinFyrGln 298				

Db	686 AGCAAGGACATACTGGCCACAGTGTGAAATAAGACATTCTGCCAATACCAAG 627	Qy	299 HistYnMetIleLeuProLeuLeuProLeuAlaArgTyrSerTrpThrPheGlySerLeu 318	Db	626 CATCTGTTCTTCATGGTCAGTGTATTTCGCCGTGGTAGTGGCTTGGCTGG 567	Qy	319 LeuPheThrPheAsnProAspLeuSerThrLysGlyLeuIleGluLysGlyThrVal 338	Db	566 AGATATAACCTCTACAGCAGTGTCTACCTGTGACAGGTGTTGGAGAACCTGTT 507	Qy	339 AlaPheHisTyrAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGlyValAlaLys 358	Db	506 CTGTTTCACTACTTTGGTTCGGACAGCGGTGCTACATCTTCTCCCTGGT---TGGAG 450	Qy	359 ProLeuAlaTrpMetValAlaThrGluLeuAlaGlyLeuIleGlyPheValPhe 378	Db	449 CCATTAGTAGATGGATGGTGCGGTGACTGAGCTGGCATGGCTGGCTGGCTGGCACAG 330	Qy	379 TирLeuSerHisAsnGlyLysGluValTyrAsnGluSerLysAspPheValArgAlaGln 398	Db	389 GTACTTAGGCCACRTGCGGTGACTGAGCTGGCATGGCTGGCTGGCTGGCACAG 330	Qy	399 ValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeu 418	Db	329 ATCGTATGCCACACGGGATATCAAGGAACATATTCAACGACTGGTTCACTGGGCCTT 270	Qy	419 AspThrGlnIleGluHisIleLeuPheProThrMetProArgHisAsnTyrProLysIle 438	Db	269 AACAGGCAAATAAGTCATCATTTCCCACATGCCCCAGGCATAATTAAACAAATA 210	Qy	439 AlaProGlnValGluIleLeuCysLysLysGlyLeuGluTyrAspAsnValSerVal 458	Db	209 GCACCTAGTGGAGGTGTTCTGTAAGAACACGGGTCTGGTAGGAAGACGGTATCTAT 150	Qy	459 ValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGluAlaSerIle 478	Db	149 GCTACCGGGCACTTGCAGGTGTTGAAAGCATTTGAGGAAGTCGGC--GAGGCTGCCA 93	Qy	479 ArgLeuHisIleAla 482	Db	92 GAGCAGGATGCT 81
RESULT 4 BJ597842/c	LOCUS BJ597842 728 bp mRNA linear EST 22-OCT-2003	DEFINITION BJ597842 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata. Physcomitrella patens	ACCESSION BJ597842.1 GI:37839834	VERSION EST	SOURCE Physcomitrella patens subsp. patens	ORGANISM Eukaryota; Viridiplantae; Streptophyta; Bryophyta; Embryophyta; Bryopsida; Funariales; Funariaceae; Physcomitrella.	REFERENCE Nishiyama, T., Fujita, T., Seki, M., Nishide, H., Shinohzaki, K., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Basebe, M.	TITLE Comparative genomics of Physcomitrella patens Gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)	MEDLINE 22709184	PUBMED 12808149	COMMENT Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp	Qy	406 LysArgGlyTrpPheAsnAspTrpPheThrGlyGlyLeuAspThrGlnIleGluHistHis 425	Db	369 AAAGGAAACATAATTCAACGACTGTTCACTGGCCCTAACAGGCAATTAGAGCCTCAT 310	Qy	426 LeuPheProThrMetProArgHisAsnTyrProLysIleAlaProGlnValGluAlaLeu 445	Db	309 CTTTCCCAAACAAATGCCAGCAATAATTAAACAAAATAGCACCTAGAGTGGAGGTGTC 250																					

Score: 583.00 Matches: 113
 Percent Similarity: 72.19% Conservative: 22
 Best Local Similarity: 60.43% Mismatches: 50
 Query Match: 22.47% Indels: 2
 DB: 2
 Gaps: 2

US-09-980-468-2 (1-483) x BJ599570 (1-697)

QY 446 CysLysHisGlyLeuGlutyrAspAsnValSerValValGlyAlaSerValAlaVal 465
 DB 249 TGTAGAAACACGGTCTGGTGTACGAAGACGTATTCATTGCTAACGGCAAGGT 190

QY 466 ValLysAlaLeuLysGluIleAlaAspGluAlaSerIleArgLeuHisAla 482
 DB 189 TTGAAAGCATTGAGGAAGTCSCG--GAGGTGCCAGAGCCAGCATGCT 142

RESULT 5
 LOCUS BJ599570/C 697 bp mRNA linear EST 22-OCT-2003
 DEFINITION BJ599570 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn26k05 3', mRNA sequence.
 ACCESSION BJ599570
 VERSION BJ599570.1 GI:37841562
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens
 Physcomitrella patens subsp. patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryopsida; Funariales; Funariaceae; Physcomitrella.
 REFERENCE 1 (bases 1 to 697)
 AUTHORS Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchihayama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 TITLE Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 MEDLINE 22729184
 PUBMED 12808149
 COMMENT Contact: Tadasu Shin-i
 Center For Genetic Resource Information
 National Institute of Genetics
 1111 Yata, Mishima, Shizuoka 411-8540, Japan
 Tel: 81-559-81-6856
 Fax: 81-559-81-6855
 Email: tshini@genes.nig.ac.jp

A backbone of the vector is basically from pBluescript II (KS'), that was in vivo excised from a 1-PLC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XbaI was ligated to Sall site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGGATCCAACCTGggAGAGTTTTTTTN-3' was used as a 1st 3' primer, and 5'-gggTCTCGAGTCATCGCTGTTCCAGACAGCAGCTGAGACTCGAGAACGGNNNN-3' as 2nd 5'-hairpin primer, giving the following 5' boarder sequence, AGGCCAAATCGGGAGCTGCTGAATTGCTGGAGAACGGACCG). cDNA insert could be amplified with conventional T7 and T3 primers. This full-length cDNA library was generated according to the method described in Nishiyama et al. (2003).
 Protonemata were blended by the POLYTRON, and then cultivated on the BCDATG medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (<http://www.brc.riken.go.jp/lab/epd/eng/index.html>). The database of Physcomitrella EST clones is available at the PHYSCObase (<http://moss.nibb.ac.jp/>).

FEATURES
 Source
 /organism="Physcomitrella patens subsp. patens"
 /mol_type="mRNA"
 /sub_species="patens"
 /db_xref="taxon:145481"
 /clone="pphn26k05"
 /tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata"
 /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"

ORIGIN
 Alignment Scores:
 Pred. No.: 5.93e-60 Length: 697

Score: 583.00 Matches: 113
 Percent Similarity: 72.19% Conservative: 22
 Best Local Similarity: 60.43% Mismatches: 50
 Query Match: 22.47% Indels: 2
 DB: 2
 Gaps: 2

QY 296 GlnTyrGlnHistidylMetIleLeuProIleLeuPheMetAlaArgTyrSerTrpThrPhe 315
 DB 696 CAATACCGCATCTGTTCTCATGGCTCTTGCCTAGTGTGGCTCTT 637

QY 316 GlySerLeuIlePheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLys 335
 DB 636 TGAGCTGGAGATACTCTACAGCASTGCTCACCTGTCACAGGTTGGAGAAG 577

QY 336 GlyThrValAlaPheHistidylAlaTrpPheSerTrpAlaAlaPheHisIleLeuProGly 355
 DB 576 GAACAGTGTCTGTTCACTACTTTGGTTCATGTCATGGCTGGACAGGCGCTATCTCTCTGGT 517

QY 356 ValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGlyLeuLeuLeuGly 375
 DB 516 --TGGAAAGCCATTAGTAGATGGATGGCTGACTGAGCTCATGTCATGGCTGGCG 460

QY 376 PhenylPheThrLeuSerHisAbnGlyLysGluValTyrAsnGluSerLysAspPheVal 395
 DB 459 TTGTGTATTGTACTTAGCCACATGGATGGGGTTTATAATTGGCTTAAGAAATTCTGTG 400

QY 396 ArgAlaGlnValIleThrThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThr 415
 DB 399 AGTGCACAGATCGTATCCACGGGATATCAAGAAACATATTCAACGACTGTTCACT 340

QY 416 GlyGlyLeuAspThrGlnIleGlyIleHisIleLeuPheProThrMetProArgHisAsnTyr 435
 DB 339 GGTCGCCTTAACAGGCAAAATAGGCATCATCTTTCACAAATGCCAGGCATAATTAA 280

QY 436 ProLysIleAlaProGlnValGluAlaLeuCysLysLysIleGlyLeuGlyAspAsn 455
 DB 279 AACAAATAAGCACCTAGTCAGTGGCTGTTCTGTAAAGAAACACGGTCTGGTGTACGAGAC 220

QY 456 valSerValValGlyAlaSerValAlaValValLysAlaLeuLysGlyLeuAlaAspGlu 475
 DB 219 GTATCTATTGCTACCGGACTACGGCAACTTGAAGGTTTGAAGGAAAGCATTTGAGGGAAAGTCGGC---GAG 163

RESULT 6
 LOCUS BJ604593/C
 DEFINITION BJ604593 normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata Physcomitrella patens subsp. patens cDNA clone pphn31g10 3', mRNA sequence.
 ACCESSION BJ604593
 VERSION BJ604593.1 GI:37846585
 KEYWORDS EST.
 SOURCE Physcomitrella patens subsp. patens
 ORGANISM Physcomitrella patens subsp. patens
 TAXONOMY Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
 REFERENCES 1 (bases 1 to 698)
 AUTHORS Nishiyama, T., Fujita, T., Shin-i, T., Seki, M., Nishide, H., Uchiyama, I., Kamiya, A., Carninci, P., Hayashizaki, Y., Shinozaki, K., Kohara, Y. and Hasebe, M.
 TITLE Comparative genomics of Physcomitrella patens gametophytic transcriptome and Arabidopsis thaliana: implication for land plant evolution
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (13), 8007-8012 (2003)
 MEDLINE 22709184
 PUBMED 12808149
 COMMENT Center For Genetic Resource Information

National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp	Db 339 CGTGGCTTAACAGGCAAATAGAGCATCATTTCCCAACAATGCCAGGCATTTA 280 Qy 436 ProLysIleAlaProGlnValGluAlaLeuCysLysLysIleGluGluThrAspAsn 455 Db 279 AACAAATAGCACCTAGTGGAGGTCTGTAAAGAACACGGCTGGTGGAGAC 220
A backbone of the vector is basically from pBluescript II (KS), that was in vivo excised from a 1-FUC phage vector (Carninci et al. 2001). 5' end of the cDNA that was digested with XbaI was ligated to SalI site of the vector and the 3' end including polyA tail was ligated to BamHI site of the vector (5'-GAGAGAGAGGATTCCACCCCTggAGAGTTCAGTGGAGCTGAGACAGCAGCTGAAATTCTCGAATCGTGAATTCTCGAGAAACCG). cDNA insert could be amplified with conventional 5' and 3' primers, giving the following 5' border sequence, AGGCCAAATGGCCGAGCTCGAATTCGTAATCGTGAATTCTCGAGAAACCG. cDNA library was generated according to the method described in Nishiyama et al. (2003). Protonemata were blended by the POLYTRON, and then cultivated on the BCDAES medium for 13-14 days under the continuous light. These clones are available from RIKEN Bio Resource Center (http://www.brc.riken.go.jp/lab/epd/Eng/index.html). The database of Physcomitrella EST clones is available at the PHYSCObase (http://moss.ncbi.ac.jp/).	Db 456 valSerIvalValGlyAlaSerValAlaValValLysAlaLeuLysGluIleAlaAspGlu 475 Db 219 GATCTATTTGCTACCGGCACTTGCAAGGTTTGAAAGCATIGAAGGAAGTCGCG---GAG 163 Qy 476 AlaSerIleArgLeuHisAla 482 Db 162 GCTGGGGAGGAGCAGATGCT 142
FEATURES	RESULT 7 LOCUS AY103762 1764 bp mRNA linear HTC 16-OCT-2002 DEFINITION AY103762 1764 mRNA sequence. ACCESSION AY103762 VERSION AY103762.1 GI:21206840 KEYWORDS ETC. SOURCE Zea mays ORGANISM Zea mays Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade: Panicoideae; Andropogoneae; Zea.
source	REFERENCE 1 {bases 1 to 1764) AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tirgey, S.V. TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes JOURNAL Unpublished (2C02) REFERENCE 2 {bases 1 to 1764) AUTHORS Coe, E.H. TITLE Direct Submission JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org ; ZmDB, www.zmdb.iastate.edu ; TIGR, www.tigr.org ; or NCBI, www.ncbi.nlm.nih.gov . When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu .
Location/Qualifiers	FEATURES source /organism="Physcomitrella patens subsp. patens" /mol_type="mRNA" /sub_species="patens" /db_xref="taxon:145481" /clone="ppbn31910" /tissue_type="mixture of chloronemata, caulonemata and rhizoid-like protonemata" /clone_lib="normalized full length cDNA library, chloronemata, caulonemata and rhizoid-like protonemata"
ORIGIN	Alignment Scores: Pred. No.: 5.95e-60 Length: 698 Score: 583.00 Matches: 113 Percent Similarity: 72.19% Conservative: 22 Best Local Similarity: 60.43% Mismatches: 50 Query Match: 22.47% Indels: 2 DB: 12 Gaps: 2
Qy 296 GlnTyrglnHistYrrMetIleLeuProLeuLeuPheMetAlaArgTyrSerTrpTrpHe 315 Db 696 CAATACAGCATCTGGTCTCATGGGTCTGTATTTCTGGTAGTGGCTCTTT 637	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
Qy 316 GlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLys 335 Db 636 TGGAGCTGGAGATAACCTCTACAGCAGTCTGACAGGGTTGGAG 577	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
Qy 336 GlyThrValAlaPheHisTyrAlaTrpHeSerTrpAlaAlaPheHisIleLeuProGly 355 Db 576 GGAACTGTTCTGTTCACTACTTGGITGCTGGACAGGGATGGAGTTATACTCTCCCTGT 517	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
Qy 356 ValAlaLysProLeuAlaTrpM MetvalAlaIleThrGluLeuValAlaGlyLeuLeuGly 375 Db 516 ---TGGAAAGCCATTAGTATGGTGGGGTGAATGGCTCATGTCGGCATGTCGGTGGGGC 460	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
Qy 376 PheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluUserLysAspPheVal 395 Db 459 TTTGTATTGTRACTAGCCACATGGGATGGAGTTATACTGCTAAAGAATTCTGTG 400	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
Qy 396 ArgAlaGlnIleValIleThrArgAsnThrLysArgGlyTrpPheAsnAspTrpPheThr 415 Db 399 AGTGCACAGATCGTATCCACACGGGATATCAAAGAACATATTCAACGACTGGTCACT 340	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."
Qy 416 GlyGlyLeuAspThrGlnIleGluHisIleLeuProLeuProArgHisAsnTyr 435 Db 45 CCPAATCAGGACCAACCACAGGCACTCGAGCC-----ACGGCCGGCA-----TGC 92	Length: 1.1764 /organism="Zea mays" /mol_type="mRNA" /db_xref="MaizedBB: 634923" /clone_lib="Maize Mapping Project/DuPont Cornsensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project."

51 ArgGlnArgSerValGlnAspLysLysProGLY----- 61
 93 CCGCTCTGCGATGCAATGCCGACGGCGGAGGGGACGTGGC 151
 62 ThrTyrSerLeuAlaAspValAlaSerHisAspArgProGlyAspCystrpMetIleVal 81
 152 ATGATCTCTCCAAAGGAGCTCCGGCTCACGGTCCGGACACTGGATCTCCCATC 211
 82 LysGluLysValItyAspIleSerArgPheAlaAspAspHisProGlyGlyThrVal--- 100
 212 TCCGGCGAAGCTACGAGTCAGCGCTGGTCCGGACCTCCCG 271
 101 IleSerThrTyrPheGlyArgAspGlyThrAspValPheAlaThrPheHisProProAla 120
 272 CTTCCTAACCTGGCCACGGCCACGGAGCCGAGGGCAGGA 331
 121 AlaTrpLysGlnLeuAsnAspTyrTyrileGlyAspLeuAlaArgGluGluProLeuAsp 140
 332 GCGGCCGCTCCTCGCCGCTCTCGTGGCCGCTCTCT---GACTACGCCGTCTCC 388
 141 GluLeuLeuLysAspTYTargAspMetArgAlaGluPheValArgGlnGlyLeuPheLys 160
 389 CCCGGTCTGCCGACTACGGCCGCTCTCGGCAGCTATCCTCCGGCCCTCTTGA 448
 161 SerSerLysAlaTrpPheLeuGlnThrLeuIleAsnAlaAlaSer 180
 449 CGCGTGGCCCCACCCCAAAGGTCCAGCTCGTCTGCTGCGCTCTCTACGCCCG 508
 181 IleAlaThrIleCystyraspLysSerTyrrpAlaIleLeuSerAlaSerLeuMet 200
 509 CTGTACCTCTGTCATGCCATGCCACCTCTCGGGCTCTCAT 568
 201 GlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPheLeuHisGlnGlnValPhe 220
 569 GGCTTCGTTCTGGATCAGTCAGTCCGGCTGGATGGGACACTCGGGCCACACCGCATCAC 628
 221 GluAsnArgThrAlaAsnSerPhePheGlyTyrIlePheGlyAsnCysValLeuGlyPhe 240
 629 AGCCATCCGGTCCCTCGACCGCGTCTCCGGAAACTGCCCTCACCGGCCCTC 688
 241 SerValSerTrpTrpArgThrLysHisAsnIleHisIleThrAlaProAsnGluCysAsp 260
 689 AGCATCGCTCTGGAAAGTGTAAACCAACAGCACACATGCCAACAGGCCCTGGAC 743
 261 GluGlnTyrThrProLeuAspGluAspIleAspThrLeuProIleAlaTrpSerIys 280
 749 CAT-----GACCCGGACCTCTCAGCACATGCCGCTCTGGCTCCCCC 793
 281 GluIleLeuAlaThrValGluSerLysArgIleLeuArgValLeu----- 295
 794 AAGCTGTTGGCAACATAATGGTCCCTACTTCAACGACCCCTGGGTTCGATGCCGCC 853
 296 -----GlnTyrGlnHistYMetIleLeuProLeuPheMetAlaArg 310
 854 TCGAAATTCTTCATCAGCTACCGACTGGACCTCTACCCGGTAATGTGCATGCCAACGG 913
 311 TyrSerTrpThrPheGlySerLeuLeuAspPheAsnProAspLeuSerThrThrLys 330
 914 ATATATCTCTCGGCAGTCGCCCTGTTCTCACG---GAGAAAGAGGGTGGCCAG 970
 331 GlyLeuIleGluLysGlyThrValAlaPheHistYAlaTrpPheSerTrpAlaAlaPhe 350
 971 CGGTGCTGCTGAGATGCCGACATTCCTGGGTGGTACCCG----- 1018
 351 HisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAla 370
 1019 -----TIGCTGGTGGCTTCCTGCCGAATTTGGTGGG-----GAGGGGTCGGG 1060
 371 GlyLeuLeuGlyPheVal-----PhthrLeuSerHis 382
 1061 TTGTGCTTTCAAGCTTCAACATCTCGGGATTCAAGCACGTCCTGAACACCAC 1120

Qy 363 AsnGlyLysGluValIty-----AsnGluSerLysAspPheValArgAlaGlnVal 399
 Db 1121 TTCTCGTCCAACTCGTATGTCGEGGCCACCCAAAGGGCAATGACTGGTTGAGAAGCAGAC 1180
 Qy 400 IleThrThrArgAsnThrLysArgGlyTyrTrpPheAsnAspTrpPheThrGlyGlyLeuAsp 419
 Db 1181 GCAGGCACGGTCGACATCCCTGCTCCTCTGGATGGTCCACGGTGGCTGCAG 1240
 Qy 420 ThrglnIle3IuHishiLeuPheProChrMetProArgHisAsnTyrProLysIleAla 439
 Db 1241 TCCAGATTGGACCATCTGTTTCCCGCTAACCTTCGCAAGGGTGC 1300
 Qy 440 ProGlnValGluAlaLeuCysLysLysGlyLeuGlyTyrAspAsnValSerValVal 459
 Db 1301 CCGGCCGTCGGACCTTSGAGGATGGCTACTTATTCTGACCCACATTCTGG 1363
 Qy 460 GlyAlaSerValAlaValValIlySAlaLeuLysGluIleAlaAspGluAla 476
 Db 1361 GGTGCAAATGTCGTTACATGGAAAGGACACTCAGGGTGTGCATTGAGGCC 1411

RESULT 8
 BQ040185 LOCUS BQ040185 519 bp mRNA linear EST 17-APR-2002
 DEFINITION gd12e11.y1 MOSS EST library PPS Physcomitrella patens cDNA clone
 PEP SOURCE ID:PPS40921 5' similar to TR:Q9ZNW2 Q9ZNW2
 DELTA6-ACYL-LIPID DESATURASE .; mRNA sequence.

ACCESSION BQ040185
 VERSION BQ040185.1 GI:19784503
 KEYWORDS EST.
 SOURCE Physcomitrella patens
 ORGANISM Physcomitrella patens
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Funariales; Funariaceae; Physcomitrella.
 REFERENCE 1 (bases 1 to 519)
 AUTHORS Quatrano,R., Bashiardes,S., Cove,D., Cuming,A., Knight,C., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Steptoe,M., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
 TITLE Unpublished (1999)
 JOURNAL Other ESTs: gd12e11.x1
 COMMENT Contact: Ralph Quatrano
 Leeds/Wash U Moss EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Libraries were constructed by Dr. Stavros Bashiardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 High quality sequence stop: 421.
 Location/Qualifiers 1. .519
 /mol type="mRNA"
 /db xref="taxon:3218"
 /clone "PEP SOURCE ID:PPS40921"
 /dev stage="protonemata, 7day old untreated"
 /lab host="E.coli DH10b"
 /clone lib="Moss EST library PS"
 /note="vector: pBluescript SK-, Site 1: XbaI; Site 2:
 EcoRI; Library constructed by Stavros Bashiardes and re-arrayed by A. Cuming & Honglin Rong. Construction of the cDNA library was carried out using Statagene's 'UniZAP - CDNA synthesis kit' to ligate cDNA directionally in UniZAP XR vector arms. The vector is designed containing the pBluescript sequence as well as the lambda DNA and cDNA is cloned in the EcoRI and XbaI sites in the pBluescript sequence. The vector was then packaged using

Gold gigaPackaging extracts, propagated in XL-1Blue MRF cells and amplified. The library was excised by mass excision using Stratagene's Mass excision kit to infect ssCIR cells with phagemids and ampicillin resistant transformants selected. Approximately 1,000,000 colonies were grown and recovered by using Qiagen midi prep kit. 2 micro grams of plasmid DNA were used to transform DH10B cells by electroporation. Clones corresponding to abundant transcripts were identified by colony hybridization and eliminated from the library, be rearrraying. This library is non-directionally cloned."

— 1 —

ignment Scores:
ed. No.:
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ery Match:
.

-09-980-46B-2 (1-483) x BQ0401B5 (1-519)
 312 SerTrpThrPheGlySerLeuLeuPheThrPheAsnProAspLeuSerThrThrLysGly 331
 4 AGTGGCTCTTTGGAGCTACAGCAGTGCTCACCTGTCACAGCAGTGCTCACCTGACAGG 63
 332 LeuIleGluLysGlyThrValAlaPheHistYrAlaTrpPheSerTrpAlaAlaPheHis 351
 64 TTGTGGAGAAGGGAACTGTTCACTACTTTGGTTCGTGGACAGCGGTGCTAT 123
 352 IleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuValAlaGly 371
 124 CTTCTCCCTGGT---TGGAAAGCCATTAGTATGGATGGCGGTGACTGAGCTCATGTCGGGC 180
 372 LeuLeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyrAsnGluSer 391
 181 ATGCTGCTGGTTTGTTATTGGTACTTAGCCACAATGGGATGGTTATAATTGCTCT 240
 392 LysAspPheValArgAlaGlnValIleThrArgAsnThrLysArgGlyTrpPheAsn 411
 241 AAAGAAATTGCGTGAAGTCACAGATCGTATCCACACGGGATATCAAGGAAACATATTCAAC 300
 412 AspTrpPheThrGlyGlyLeuAspThrGlnIleGluHisIlePheProThrMetPro 431
 301 GACTGGTTCACTGGTGGCCTAACAGGCCAAATAGGCATCATTTCCAAACAATGCC 360
 432 ArgHisAsnTyrProLysIleAlaProGlnvalGluAlaLeuCysLysLysIleLeu 451
 361 AGGCATAATTAAACAAATAGCACCTAGAGTGGAAAGCTTACGGCCTATIGCTGCAAGSTTITGAAAGCATTGAAAGGAA 420
 452 GlutyrAspAsnValValGlyAlaSerValAlaValValLysAlaLeuLysGlu 471
 421 GTGTACGAAAGACGTATCTATIGCTACGGCACTTGGCAAGSTTITGAAAGCATTGAAAGGAA 480
 472 IleAlaAspGluAlaSerIleArgIleWtHisAla 482

SULT 9				
076485	AK076485	2272 bp mRNA linear	HTC 18-SEP-2003	
ICUS	Mus musculus	0 day neonate head cDNA, RIKEN full-length enriched		
DEFINITION	Mus musculus	library, clone:4833423E24 Product:unclassifiable, full insert		
		sequence.		
ACCESSION	AK076485			
VERSION	AK076485.1	GI:26096835		
KEYWORDS	HTC; CAP trapper;			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;			
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;			

AUTHORS	Carninci, P. and Hayashizaki, Y.
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	<p>AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.</p> <p>TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes</p> <p>JOURNAL Genome Res. 10 (10), 1617-1630 (2000)</p> <p>MEDLINE 20499374</p> <p>PUBMED 11042159</p>
REFERENCE	<p>AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanuki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.</p> <p>TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer</p> <p>JOURNAL Genome Res. 10 (11), 1757-1771 (2000)</p> <p>MEDLINE 20530913</p> <p>PUBMED 11076861</p>
REFERENCE	<p>AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.</p> <p>TITLE Functional annotation of a full-length mouse cDNA collection</p> <p>JOURNAL Nature 409, 685-690 (2001)</p>
REFERENCE	<p>AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.</p> <p>TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs</p> <p>JOURNAL Nature 420, 563-573 (2002)</p> <p>6 (bases 1 to 2272)</p>
REFERENCE	<p>AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Eirozane, T., Bori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T., Katoch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sanc, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takuwa-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.</p> <p>TITLE Direct Submission</p> <p>JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)</p>
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES	Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/
source	<p>1. 2272 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM_DB:4833423E24" /db_xref="MGI:2391495"</p>

misc_feature	11_2272 /note="unclassifiable"	ORIGIN	1067 ----ATCTACCCCAAGGATCAGACATTGATGGCCCCACTC-----TTCTGGTG 1114	Db
			281 GluIleLeuAlaThrValGlu---SerLysArgIleLeuArgValLeuGlnTyr---- 297	Qy
			1115 GAGATACTAGCCT-ATAAGTATGGCAAGAAATAAACATGGACTATGAGAAG 1173	Db
			298 GlnHis-----TyrMetIle---LeuProLeuLeu----- 306	Qy
			1174 CAGCACCTGTACTTCACATGGTTGCACCTCCCTCTCATGCCCTACTTAATTGG 1233	Db
			307 -----PheMetAlaArgTyr-SerTrpTrpHe---GlySerLeuLe 319	Qy
			1234 CAATCCATGCAAGTGAATGGTACCTTGAAATAACTGGATGACATTGCATGGTAGCAGC 1293	Db
			319 upheTrpHeAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGlyThrValAl 339	Qy
			1294 TTTTACATTC-----GT 1305	Db
			339 a-PheHistTyralaTrpPheSerTrpAlaAlaPheHisIleLeuProGlyValAlaLysP 359	Qy
			1306 TATTTCATCACATTTGG-----C 1323	Db
			359 roLeuAlaTrp-MetValAlaThrGluLeuValAlaAspIleLeuLeu----- 373	Qy
			1324 CCTTCTATGGAAATTTCGGAACAGTGTGCTCATATTTGGTCAAGTTATTGAGAGC 1383	Db
			374 -----LeuGlyPheValPheThrLeuSerHisAsnGlyLysGluValTyRAsn---Glu 390	Qy
			1384 CCCTGGATTTGCTTACGTACCCAGATGAGTCACATACCATGAAATGAGCAGTTGAAGAG 1443	Db
			391 SerLysAspPheValArgAlaGlnValIleThrArgAsnThrLysArgGlyTrpHe 410	Qy
			1444 AACCACGACTGGCTCAGGCACTCGGTGCTGCCCACCTCTTCCACAATG 1503	Db
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			1504 ATGACTGGTTCACTGGACATTTGAACTTCCAATTTGAAACCCACCTCTTCCACAATG 1563	Db
			431 ProArgHiAsnTyProllysIleAlaProGlnValGluAlaLeuCysIlysHiSsLY 450	Qy
			1564 CCACGCCATAATTACCECAAAAGTGCACCTCTGGTAAGTCAGTGCCTCAGCATGA 1623	Db
			451 LeuGlutYrAspAsnValSerValValGlyAlaSerValAlaValAlaLeuLys 470	Qy
			1624 TGGCAGTATAATAAGGCCATATTGAAAGGGCTTCTGGAGATATTGTCAGGTCCCTTGAAAG 1683	Db
			471 GluIleAlaAspPheValSerIleArgLeuHiSalahis 483	Qy
			1684 AAG-----TCTGCTTCCCTCTGGATGATGCTTAC 1713	Db
			RESULT 1G	
			AY418548 1335 bp DNA linear GSS 17-DEC-2003	
			LOCUS Homo sapiens FADS2 gene, VIRTUAL TRANSCRIPT, partial sequence,	
			DEFINITION Homo sapiens FADS2 gene, VIRTUAL TRANSCRIPT, partial sequence.	
			GENOMIC genomic survey sequence.	
			ACCESSION AY418548	
			VERSION AY418548.1 GI:39774508	
			KEYWORDS GSS	
			SOURCE Homo sapiens (human)	
			ORGANISM Homo sapiens	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	
			REFERENCE 1 (bases 1 to 1335)	
			AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tranenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D., and Cargill,M.	
			TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
			JOURNAL Science 302 (5652), 1960-1963 (2003)	
			PUBLMED 14671302	
			REFERENCE 2 (bases 1 to 1335)	
			AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,	

QY 283 LeuAlaThrValGluSerLysArgIleLeuArgValLeuGlnTyrGlnHisTyr----- 300
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 Db 768 CTTCCCTGGAGCTGGAGAACAGAAAGCACTGCCATACCAACCATCAGCACAG 827

QY 301 -----MetIleLeuProLeuLeuPhe----- 307
 Db 828 TACTTCCTCCTCATGGACCCAGCCCTTGCTGCCTCTATACTCCAGTGGTATAATTTC 887

QY 308 -----MetAlaArgTyrSerTrpThr-----PheGly 316
 Db 888 TATTTGGTTCTAGCGGAAAAAATGGGGACTTGGCCTGGATEGTCAGCTCTATGCC 947

QY 317 SerLeuLeuPheAsnProAspLeuSerThrThrLysGlyLeuIleGluLysGly 336
 Db 948 CGCATCTCTTCACTTACATGCCGCTGCTG-----AAAGGC 989

QY 337 ThrValAlaPheHistYrAla-----TrpPheSerTrpAlaAla 349
 Db 990 TTCCCTGGCCTTTCTCATTGTCAAGGTTCCTGGAAAGCAAAC 1043

QY 350 PheHisIleLeuProGlyValAlaLysProLeuAlaTrpMetValAlaThrGluLeuVal 369
 Db 1043 ----- 1043

QY 370 AlaGlyLeuLeuLysGlyPheThrLeuSerHisAsnGlyLysGluVal---Tyr 388
 Db 1044 -----GTCGACACAGATGAACCATATCCCACATTGACACATTGATCAC 1082

QY 389 AsnGluSerLysAspPheValArgAlaGlnValLeuThrThrArgAsnThrLysArgGly 408
 Db 1083 GACCGGGATGTGGACCTGGTCCTCACCAGCTGCAGGGCAACCTGCAACATTCA 1142

QY 409 TrpPheAsnAspTrpPheThrGlyGlyLeuAspPTrgInIleGluLysHisLeuPhePro 428
 Db 1143 GCCTCAACAACACTGGTCAGTGGCCACCTAAATTCCAGATTGAACACCACCTCTCCCC 1202

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QY 449 HisGlyLeuGluTyrAspAsnValSerValAlaValValLysAla 468
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QY 469 IleLysGlu 471
 Db 1323 CTGAAGGGAG 1331

RESULT 12
 SOURCE AW476747/c
 ORGANISM Physcomitrella patens
 DEFINITION gaa37d12.y1 Moss EST library PPU Physcomitrella patens cDNA clone
 PEPE SOURCE ID:PPU040224 5' similar to TR:Q9ZNW2 Q9ZNW2
 DELTA6-ACYL-LIPID DESATURASE. ; mRNA sequence.
 ACCESSION AW476747
 VERSION AW476747.1 GI:7046910
 KEYWORDS EST.
 SOURCE Physcomitrella patens
 ORGANISM Physcomitrella patens
 DEFINITION Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 Bryopsida; Funariales; Funariaceae; Physcomitrella.
 REFERENCE Quatrano, R., Bashniardes, S., Cove, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
 TITLE Leeds/Wash U Moss EST Project
 JOURNAL Unpublished (1999)
 COMMENT Contact: Ralph Quatrano
 Leeds/Wash U Moss EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

QY Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watsen.wustl.edu
 Libraries were constructed by Dr. Stavros Bashniardes as part of the Physcomitrella EST program (PEP) at the Univ. of Leeds (UK) and Washington Univ. in St. Louis (USA) DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Celia Knight (c.d.knight@leeds.ac.uk)
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco
 High quality sequence stop: 412.

Location/Qualifiers
 1. .622
 /organism="Physcomitrella patens"
 /mol_type="mRNA"
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 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XbaI; Construction of the cDNA library was carried out using Stratagene UniZAP - cDNA synthesis kit. cDNA was constructed using an oligo dT primer/linker that contains a XbaI site within it. Following ds cDNA synthesis, EcoRI adaptors were ligated to the blunt ends with XbaI. The result is cDNA with an EcoRI sticky end on one side and a XbaI sticky end on the other. This cDNA was ligated directionally in UniZAP arms. The vector is designed containing the pBluescript sequence as well as lambda DNA and cDNA is cloned within this pBluescript sequence. The vector was then packaged using Gold gigapackaging extracts. Library was grown in XLIBlue MRF' cells and amplified. The library was excised by mass excision using Stratagems 'Mass excision kit' that uses exo nuclease as a helper phage that releases the pBluescript sequence and circularises it as single stranded plasmids that are then packaged (by helper phage) and secreted out of the host cell as phagemids. SCOR cells were transformed with phagemids and the library was plated out on LB-amp plates to select for transformants. Approximately 1,000,000 colonies were grown and recovered. The double stranded plasmid library was recovered by using Qiagen Midi prep kit. 2 micro grams of each library were used to transform DH10B cells by electroporation."

ORIGIN
 Alignment Scores:
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 Score: 517.00
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 Best Local Similarity: 62.58%
 Query Match: 19.92%
 DB: 10
 Gaps: 2

US-09-980-468-2 (1-483) x AW476747 (1-622)
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 Gaps: 2

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QY 368 LeuValAlaLysIleLeuLeuGlyLeuSerHisAsnGlyLysGluVal 387
 Db 485 CTCATGCCGCATGCTGGCTTGTATTGTACTAGCCACATGGGAGCTGTT 426

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425 TATAATTCTAARGAATTCTGAGTCACAGATCGTGCACAGATGGATATCCAAAGGA 366
 Db Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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 Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
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 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.

408 GlYTrpPheAsnAspTrpPheThrGlyLeuAspThrGlnIleGluHisLeuPhe 427
 Qy 365 AACATATTCAACGACTGGTTCACTGGGCCAACAGGCAAATAGGGCATCTCTTC 306

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Db 468 AlaLeuIysGluLLeAlaAspGluAlaSerIleArgLeuHisAla 482
 Qy 185 GCATTGAAAGGAAGTCGCG--GAGGCTGCGCAGAGCAGCATGCT 144

Db 1689 CDNA library was prepared and sequenced in Mouse Genome
 Direct Submission Encyclopedia Project of Genome Exploration Research Group in Riken
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan {E-mail: genome-res@gsc.riken.go.jp},
 URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222,
 Fax:81-45-503-9216

COMMENT CDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in Riken
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL:<http://genome.gsc.riken.go.jp/>
 URL:<http://Fantom.gsc.riken.go.jp/>.

FEATURES Location/Qualifiers

source 1. /organism="Mus musculus"
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 WNFHRHFOBHAKPNIFHKDPDVTVAPVFLGESSVEYGGKKRRLPYNHQHLYPFLIGP
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ORIGIN

Alignment Scores:
 Pred. No.: 4.18e-51 Length: 1689
 Score: 516.00 Matches: 138
 Percent Similarity: 47.39% Conservative: 71
 Best Local Similarity: 31.29% Mismatches: 166
 Query Match: 19.88% Indels: 66
 DB: 11
 Gaps: 17

US-09-980-468-2 (1-483) x AK080414 (1-1689)

Qy 68 ValAlaSerHisAspArgProGlyAspCystrpMetIleValLysGluLysValtyrAsp 87
 Db 130 ATCCGCCAGCATGACCTACAGGGCACAAAGTGGCTGATCGAGGCCGTCATGAGCTGCTACGAC 189

Qy 88 IleSerArgPheAiaAspAspHeisProGlyGlyThr--ValIleSerThrTyrPheGly 106
 Db 190 ATAGCCGGTGGGCACAGGGCACCCAGGGCACAGGGCACATGGCCCTCATGGCCACCACGGTSGC 249

REFERENCE The FANTOM Consortium and the RIKEN Genome Exploration Research
 AUTHORS Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 REFERENCE Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Fukuda, S., Furuno, M., Hanaoka, T., Hara, A., Hashizume, W., Hirozane, T.,
 Hayashida, K., Hayatsu, N., Hiraoka, T., Hiramoto, K., Hiraoka, T., Hirozane, T.,

5 20530913
 REFERENCE PUBMED 11076861
 4 The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE JOURNAL Nature 409, 1757-1771 (2000)
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
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 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation

QY	107 ArgAspGlyThraspValPheAlaThrPheHisProProAlaAlaTrp----LysGln 124	Db	1234 ACTACCGAGGGTGGCCCTCTGGTCAGGCCAGGCTACACTAC 1293
Db	250 GAGGACGCCACGGGAracCCTCCACGCCTTCCACCAAGATCTCCATTGTGCAAGTTC 309	QY	454 AspAsnValSerValValGlyAlaSerValAlaValLysAlaLeuLysGluIleAla 473
QY	125 LeuAsnAspTyrIleGlyAspLeuAlaArgGluGluProLeuAsp---- 140	Db	1294 GAGGTGAAGGCCCTTCCTCACCGCTCTGGTGGATATCATGGGTCCCTGAAGAGTCTGGC 1353
Db	310 CTGAAACCCCTGTTGATGGAGCTAGGCCAGAGCTAGGCCAGAGCTAGGCCAGGATGGCTAG 369	QY	474 Asp 474
QY	141 -----GluleuLeuLysAspTyryArgAspMetArgAlaGluPheValArgGluGlyLeu 158	Db	1354 GAC 1356
Db	370 AATGCCAACGCTGATGGAGCTTCCGAGCCTTGCCAGGCCAGCTGAAGACATGAAGCTG 429		RESULT 1.4
QY	159 PheLyssSer-LysAlaTrpHe---LeuLeuGlnThrLeuIleAsnAlaAlaLeuPhe 177	Db	AK029318 LOCUS AK029318 3129 bp mRNA linear HTC 18-SEP-2003
Db	430 TTGGAAGCTGATGATGACTTCTTGCACCTCTGGCTCCTGGCTATGGAGTRG 489		DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832423A09 product:fatty acid desaturase 3, full1
QY	178 AlaAlaSerIleAlaThrIleCystyAspLysSertTytrpAlaIleValLeuSerAla 197	Db	AK029318 ACCESSION AK029318.1 GI:26325277
	490 TGGCCTGGCTTATCATCTACCTCTGGCCCTGGCTGGGTGTCAGTCTGGTCTGCC 549		VERSION HTP; CAP trapper.
QY	198 SerLeuMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPheLeuHisGln 217	Db	ORGANISM Mus musculus (house mouse)
Db	550 CTGATCTGGCCATCTCTCGGCCAGTCTGGTGTGCAACATGATCTGGTCATGCC 609		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
QY	218 GluValPheGlu-----AsnArgThrAlaAsnSerPhePheGlyTyrrLeuPhe 233	Db	1 Carninci, P. and Hayashizaki, Y.
Db	610 TCCATCTTCACTAAGTCCAGGTGGAAACCATGTGGCCAGGAGTTC-----GTGATG 660		2 Carninci, P. High-efficiency full-length cDNA cloning
QY	234 GlyAsnCysvalLeuGlyPheSerIleTrpPargThrLysHisAsnIleHisHis 253	Db	AUTHORS Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Db	661 GGGCAG---TTGAAAGGCTTTCGGCCACTGGGAAATTTCGGCCACTTCAGCRCCAT 717		JOURNAL Meth. Enzymol. 303, 19-44 (1999)
QY	254 ThrAlaProAsnGluCysAspPheGlnTyrrProLeuAspGluAspIleAspThrLeu 273	Db	99279253 REFERENCE 2
Db	718 GCCAAACCAACATCTTCCACAA-----GACCCAGATGTGACTGTGCGCA 762		AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Iwasa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, S., Matsuo, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
QY	274 ProIleLeuAlaTrpSerIleGluIleLeuAlaThrValGluSerLysArgIleLeuArg 293	Db	TITLE Genome Res. 10 (10), 1617-1630 (2000)
Db	763 CCTGTCCTCCTCTGGGGAGTCATCTGGAGTATGGCAAGAGAAACG-----AGA 816		PUBMED 20499374
QY	294 valLeuGlnTyrglrrHs-----TyrMetIleLeu-----ProLeuLeuPhe 307	Db	3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Iwasa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, S., Matsuo, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Db	817 TACCTGCCCTACACCAACGAGCATCTATACTCTTCCTCGATTGCCCTCGCTCAC 876		4 RIKEN integrated sequence analysis (RISA) system--384-Format sequencing pipeline with 384 multicapillary sequencer
QY	308 MetAlaArgFyr-----SerTrpThrPhe 315	Db	Genome Res. 10 (11), 1757-1771 (2000)
Db	877 TGGTGAACTTGAAAGTTGACATGGTGTGCAATGCTGGCATGGCATGGACG--- 933		PUBMED 20530913
QY	316 GlySerLeuLeuPheThrPheAspProAspLeuSerThrThrLysGlyLeuLeuGly 335	Db	5 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujikawa, S., Inoue, K., Togawa, Y., Iwasa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, S., Matsuo, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
Db	934 ---GACTTGCTGTGG----- 945		6 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs (bases 1 to 3129)
QY	336 GlyThrvalAlaPheHistTyrrAlaTrpPhe---SerTrpAlaAlaPheHisIleLeuPro 354	Db	7 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection
Db	946 ---GCTGCCAGTTCTACTCCGCTTTCGCTCTACTCTCCCTCTAT----- 993		Nature 409, 685-690 (2001)
QY	355 GlyvalAlaLysProLeuAlaTrpMetValAlaLysGluLeuValAlaGlyLeuLeu 374	Db	8 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs (bases 1 to 3129)
Db	994 GGTGCCACTGGGACACTGGCTCTCTGGTCAAGGGTGGCTGGAGGCCACTGGTC 1053		Nature 420, 563-573 (2002)
QY	375 GlyPheValPheThrLeuSerHisAsnGlyLysGluValtyAsnGluSer---LysAsp 393	Db	9 Fukuda, S., Furuno, M., Hanagaki, T., Bara, A., Hashizume, N., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shiba, K., Shinagawa, A., Shiraki, T., Takaku-Akahira, S., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
QY	394 PheValLysProAspThrGlnIleGluLysIlePheProThrMetProArgHIS 413	Db	10 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Bara, A., Hashizume, N., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shiba, K., Shinagawa, A., Shiraki, T., Takaku-Akahira, S., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
QY	1114 TGGCAAGCTCAGCTGGCACCCTGCAATGTTGCTCTTCTATTGACTGG 1173	Db	11
QY	414 PheThrGlyGlyLeuAspThrGlnIleGluLysIlePheProThrMetProArgHIS 433	Db	12
Db	1174 TTGAGGGCACCTCAATTGACCACTCTTCCCACGRTGGCCAAGGCA 1233		13
QY	434 AsnTyrProLysIleAlaProGlnValGluAlaLeuCysLysIleGlyLeuGly 453	Db	14

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, N., Muramatsu, M. and Hayashizaki, Y. Direct Submission Submitted (16-CUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 235-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
 URL: http://Fantom.gsc.riken.go.jp/. Location/Qualifiers

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CDS
FEATURES
SOURCE

DNA
159 PheLysSerLysAlaTrpPhe---LeuLeuGlnThrLeuIleAsnAlaLeuPhe 177
178 AlaAlaSerIleAlaThrIleCysTyrAspLysSerTyrTrpAlaIleValLeuSerAla 197
198 SerIleMetGlyLeuPheValGlnGlnCysGlyTrpLeuAlaHisAspPheLeuBisGln 217
437 TrGGCCCTGGCTTATCATCTTCACTTCTGCACACTCGCTGGCCACATCTGGCTATGGAGTTG 496
497 TrGGCCCTGGCTTATCATCTCAGGCCATCTGCTGCAACATGATCTAGTCATGCT 556

QY
317 CTGAAACCCCTGTTGATTGGAGCTAGCCCCAGGAACCCAGCCACGGATGGCTCAG 376

DB
141 ----GluLeuLeuLysAspTyrArgAspMetArgAlaGluPheValArgGluGlyLeu 158
377 AATGCCCAAGCTGATCGAGGACTTCGAGCTTGCCAGGCTGAAAGACATGAAGCTG 436

QY
159 PheLysSerLysAlaTrpPhe---LeuLeuGlnThrLeuIleAsnAlaLeuPhe 177
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DB
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